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GenCore version 4.5
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OM protein - protein search, using sw model

September 26, 2000, 17:18:56 ; Search time 75.19 Seconds (without alignments) 104.271 Million cell updates/sec Run on:

US-09-430-029-3 Perfect score: Sequence:

1723 1 MTIELKTVDIKPLRHIFAHV.....ALDEVREQFHARAARLGIAL 331 Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

188963 seqs, 23686106 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length; 0 Maximum DB seq length; 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Descripti	H	C C C C E	TOTAGINE O	Arcaligen	Nocardia	Nocardia	pera-T':
qi		W06800	W98971	P66213	7891459	R03056	1110000
DB	1	Н	-	, <del>,</del>	- ا	-	- ا
Length		331	331	347	343	370	נענ
Query Match Length DB	1 1 1 1 1 1	74.4	48.3	10.4	10.4	5.0	C.
Score	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1282	832	179.5	178.5	86.5	×
Result No.	1 1 1 1 1 1 1	. →	7	m	4	Ŋ	9

	Describtion	Toluene orthor	) [	Mosadia com	57	ura coralli	Beta-1, 3-glucanase	Corrected Bacillus	Beta-1,3-glucanase	Tomato PR-qlucanas	Beta-1,3-qiucanase	Beta-1,3-glucanase	Beta-1.3-dlucanaco	in ancoded		Hobecon both 1 2	A protoin with it	Process Will	protein with	A protein with ste	T. niveum Cyclospo	Mycobacterium Kans	creto	$\alpha$	Streptococcus pneu	Giutamine-oxogluta	Forcine retrovirus	nermostable alk	ч		Miniature swine re	Lipase modulating	Bacillus sp. xylan	That or	Traccone synchase	5
		00		m	0	ı (c		<u>Σ</u> ι.	ų (	æ:	4	ű	80	J.	0	m	) F	ı (m	1	* 0	no	no	<i>n</i> (m	n (1	<b>4</b> %	ne	v ⊂		. [1	0 10	~ <	* 1	. ~	. 🖶	7	
qi	1	00	$\sigma$	R6621	R8146	P0305	W1070	1000	KU/31	09/7M	R0305	R0305	R14028	R2200	W83440	W7354	W8224	WR7563	WR7564	00170	W7740	100520	10000	00000	X00004	10000	R7655	W5284	94456	W3200	D1086/	W9314	R8680	26	R13277	
DB		Н	Н	Н	۲	-	-	٠,	٦.	٠,	٠,	Н	Н	-	Н	,	Н	,	-	-, ۱		- ۱	1 -	ı -	4 -	-, ۱		۱	- ا	- 1	+ -	f ,	ı —	-		
Length	1	331	331	342	343	370	7.6	100	000	700	50 C	20.0	359	359	359	359	325	329	330	15281		437	504	241	506	1194	396	1721	1810	1145	344	397	457	1611	359	
Match	1 1 1 1	4.	œ		0							•	-	-	4.9	4.9	4.9	4.9	4.9	4 9				•			•	•	4.6	4.6		•	4.5	4.5	4.4	
Score	1		832	179.5	178.5	86.5	986	ľ	) v	F =	* =		. ·		∹.	<del>.</del> .	84	84	84	84	83.5	ထ	81.5	$\alpha$	81	81	80		9.	79	7.8	7.8	7.8		76.5	
No.	1 1 1	, γ	.4	m	4	Ŋ	9	7	- ac	o	, ,	) F	77	7.7	13	14	12	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	

	NICOLIANA SP. intr	Ded ID #8 ILOW DEI	Flateholide Syntha	MOV OVE-NEET 113	Majro HDD-31:00:00	marze obragueose	malester nod	1 racione synthase	Sabingarianel ri	Spiningomonas sp. s	Murine ubiquitin-p	
W31299	W64232	W23718	W22508	R21570	W03756	R38091	W22601	W52845	W89246	W97051	W84351	
,	-	-	l r-1	-	Н	-	-	-	-	-	-	
359	1336	3724	3724	393	471	210	4472	4572	412	412	1757	
4.	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.3	4.3	4.3	
76.5	76.5	76.5	76.5	92	92	75.5	75.5	75.5	74.5	74.5	74.5	
34	32	36	37	38	39	40	41	42	43	44	45	

# ALIGNMENTS

No 6800 standard; Protein; 331 AA.  AC W06800,  W06800,  To 29-JAN-1997 (first entry)  E Toluene ortho-monooxygenase subunit tomal.  Toluene ortho-monooxygenase subunit tomal.  Toluene orthoroethylene; TCE; degradation.  PR VEXAV. 1991; 694718.  PR 02-MAY-1991; 694718.  PR 02-MAY-1991; 05 694718.  PR 02-MAY-1991; 05 694718.  PR 12-MAY-1991; 05 694718.  PR 15-DEC-1993; US-167457.  PA FRANCESCONI S C.  PA (FRAN) FRANCESCONI S C.  PA (FRAN) FRANCESCONI S C.  BA (SHIE,) SHIELDS M S.  PA (SHIE,) SHIELDS M S.  Control of chloro:alliphatic cpds. and aromatic.  BA (SHIE,) SHIELDS M S.  PA (SHIE,) SHIELDS M S.  PA (SHIE,) SHIELDS M S.  CONTROL OF CONTROL OF CHORO:alliphatic cpds. and aromatic.  CC (CMA) Hororyganisms transformed with P. cepacia PRI-23 Tom enzyme gene are useful for degradation of chloro:alliphatic cpds. and aromatic.  CC COMA! Encoded by T44457, isolated from Pseudomonas cepacia strain.  CC COMA! Encoded by T44457, isolated from Pseudomonas cepacia strain.  CC COMA! Encoded by T44457, isolated from Pseudomonas cepacia strain.  CC CTED, a hazardous pollutant. The proM plasmid is transmissable placed encoded proM. The enzyme is capable of degrading trichloroethylence corporation and second profession of constitutively degrade TCE, esp. in bioreactors or context expressable in other bacteria, thus many bacteria can be genetical altered to constitutively degrade TCE, esp. in bioreactors or context effect, in effect, on the suryme required to break down TCE, in effect, on the suryme required to break down TCE, in effect, on sequence 331 AA.		
	A) For Fig. 19. The American Annual A	Protein: 331
		(first entry)
		0-monooxyqenase subunit tomal
		elf-transmissable: cometitutive: bioxosatar:
		 richloroethylene: TCE: degradation
		cepacia strain PR1-23
		694718.
		US-694718
		US-167457
		US-319387.
		U.S. INCOSEC
		CDS M. S.
		SC, Shields Ms:
		10/37
		57.
		ns transformed with P. cepacia DR1-33 Tom common 2000
		or degradation of chlorocalishetta and and enzyme gene
		umn 27-30: 25pp: English
		sequence is that of toluene ortho-monocoxygoness and
		by T44457, isolated from Dsendomonas occasis atmain
		lom gene is present on a large self-transmissable alimit
		The enzyme is capable of degrading trickloude plasmid
		irdous pollutant. The nTOM plasmid is transmissable
		n other bacteria, this many bacteria on be accepted and
		nstitutively degrade TCE, esp in biorestor or
		ited environments p cenacia politica contention
		is chemical inducers and is canable of functioning man
		 of conditions. Also it does not require an induced that is
		 for the enzyme required to break down not in office.
		competitive inhibition.
		1. AA;

Gaps . 0 Ouery Match 74.4%; Score 1282; DB 1; Length 331; Best Local Similarity 72.9%; Pred. No. 1.4e-129; Matches 240; Conservative 32; Mismatches 57; Indels

ö

1 MIIELKTVDIKPLRHTFAHVAQNIGGDKTATRYQEGMMGAQPQENFHYRPTWDPDYEIFD 60 qq δŏ

61 PSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARA 120 δŏ QQ

δy qq

QY

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g δλ a

δğ

301

RESULT W98971 drug.

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Claim 5; Page 6-7; 11pp; Japanese.
R81469-R81472 are protein products of the Nocardia corallina strain
B-276 alkene mono-oxygenase gene. The gene encodes 4 protein products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W-----GANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLT-RLALAMAEPDVLEA-A 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 WPFVEYGLFLSLAYAVRQAMSDTVQFSVVFQAVDRMRLLQDIVHHLDHLQESPEFSDAGA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 TIPAVIASALLDSGRHLES---VQALVRLVCQDPVHGDQNQATVRRWIEBWQPRCKAAAQ 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 FYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARALDVLVPL-----RHAA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 LWQRPYVSTCNQDQQAL-----ARLVPVLTMGSAA-----ITPIWSQKILARSYAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 TRYQEGMMGAQ--PQENFHY-----RPTWDPDYEIFDPSRSAIRMANWYALKDPRQ 79
                                                                                                                                                                                              Alkene mon:oxygenase and corresp. gene - useful for the epoxidation of an alkene claim; 19 age 2; 30pp; Japanese.

Claim; 19 age 2; 30pp; Japanese.

Claim; 19 age 2; 30pp; Japanese.

E.coli transformed with the DNA sequence 079569 are able to catalyse the epoxidation of alkenes. The DNA is derived from Nocardia corallina and comprises 4 open reading frames. ORPs amoA and amoC encode subunits 1 and 2 of the alkene monoxygenase enzyme and oRP amoD encodes a reductase capable of transferring electrons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGLLYPLVYDRFVDERIALEG-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 SAVAMLTAFMPE--WHTESNRWIDAVVKTMAAE---SDDNRALLARWIRDWSARAEAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 TEYELYIVGQOSIPDEWLHYDWPLRFDDGRAPWEEE-----SSAVRISEWSAYRDPHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microbe having alkene monooxygenase activity to oxidise indole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nocardia corallina alkene mono-oxygenase gene product, amoA. Alkene mono-oxygenase; indole; indigo production; biosynthesis; microbial oxidation; dye. Nocardia corallina B-276.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 indigo by a microbiological method - by culturing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
Nocardia corallina alkene monoxygenase subunit-1.
alkene monoxygenase; subunit-1; epoxidation; amoA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 179.5; DB 1
Pred. No. 3.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 SFLPTFSDCGIDAKESANALSRALANQRAAVEGAGI 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297 -LAPVAARALQDAGRAALDEVREQFHARAARLGIAL 331
                                                                                                                                                                                                                                                                                                                                                             from NADH coenzyme to a monoxygenase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R81469 standard; Protein; 343 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55;
                                                                                                                                                                                                                                                                                                                                                                                                                                       10.4%; 22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-1996.
08-JUL-1994; 179688.
08-JUL-1994; JP-179688.
(NIHA ) JAPAN ENERGY CORP.
WPI; 96-133426/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R81469;
07-AUG-1996 (first entry)
                                                                                                                                    (NIHA ) JAPAN ENERGY CORP.
WPI; 95-009069/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                     JP-105171
                                                                                                   06-APR-1993; 105171
06-APR-1993; JP-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity
Matches 77; Conserv
                                           Nocardia corallina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T17418
                                                                                                                                                                                     079569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J08023988-A.
                                                                                21-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   indigo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
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R81469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qd
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          δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention also describes PoxA, PoxK, PoxC, PoxE, PoxE, PoxF, PoxG, PoxH and PoxI. The proteins are useful in the fields of petroleum purification, chemical industry and drug industry related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New encoding an aromatic cpd. oxidative decompsn. enzyme - useful in the fields of petroleum purification, chemical and drug industries Claim 1; Page 7-19; 35pp; Japanese.
The present sequence encodes Alcaligenes sp. protein PoxB. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAM--AEP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-MAY-1999 (first entry)
Alcaligenes sp. protein PoxB.
Alcaligenes; PoxR; PoxA; PoxB; PoxC; PoxD; PoxE; PoxF; PoxG; PoxH; PoxI; aromatic; oxidative; petroleum purification; chemical industry;
        181 IDBAKQAWMTSPDWQPLRRYVENTLVLQDPVELFIAQNLALDGLLYPMIYGAFVDDYIAL 240
                                             241 EGGSAVAMLTAFWPEWHTESNRWIDAVVKTWAAESDDNRALLARWTRDWSARAEAALAPV 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MIIELKIVDIKPLRHTFAHVAQNIGGDKTATRYQEGMMGAQPQENFHYRPTWDPDYEIFD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 DVLEAAKATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNEALDGLLYPLVYDRFVDERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 ALEGGSAVAMLTAFMPEWHTESNRWIDAVVKTMAAESDDNRALLARWTRDWSARAEAALA
                                                                  241 NGGSAVAMLITEMPEWHDESSRWUDAVVRIMATESEDNKALLIHWLRIWEDQAASALLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synthesis, conversion and decomposition of aromatic compounds. Sequence 331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.3%; Score 832; DB 1;
50.0%; Pred. No. 3e-81;
tive 49; Mismatches 113,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 PVAARALQDAGRAALDEVREQFHARAARLGIA 330
                                                                                                                                301 AARALQDAGRAALDEVREQFHARAARLGI 329
                                                                                                                                                                       AEMALAENGHDALEEVRQQLRAALRRPGL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                            AA.
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R66213;
04-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                          W98971 standard; Protein; 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-JUL-1997; 200625.
25-JUL-1997; JP-200625.
(TOFU ) TONEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               al Similarity
166; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 99-197820/17.
N-PSDB; X18867.
                                                                                                                                                                                                                                                                                                                                                                                                                Alcaligenes sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                   J11042088-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-FEB-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Best Loca Matches

qq

 $\delta \dot{\lambda}$ g QΥ

δλ

RESULT

HG HG

Op  $Q \underline{y}$ 

g QΥ

14;

Gaps

59;

8

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14;
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Beta-1,3-glucanase is involved in plant defence against pathogens and as it hydrolyses polyssaccharides, useful in biomass conversion or paper making. The clones allow for transfer of the gene to other species and control of gene expression.
amoA, amoB, amoC and amoD derived from the 3 different reading frames of the operon. The gene is useful for the production of indigo via oxidation of indole. Nocardia corallina can be cultured in a medium contg. indole and will readily oxidise the indole yielding indigo into the culture medium. E. coli may also be transformed with the alkene mono-oxygenase gene and used as above to efficiently produce indigo by microbial oxidation.
                                                                                                                                                                                                                                                                                                                                                                                                    80 FYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARALDVLVPL------RHAA 131
                                                                                                                                                                                                                                                                                                                                                 ----ITPIWSQKILARSYAA 128
                                                                                                                                                                                                                                                                                                                                                                             W-----GANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLT-RLALAMAEPDVLEA-A 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                 KATWIRDAAWQPLRRYVEDILVVADPVELFIAQNLALDGLLYPLVYDRFVDERIALEG-G 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : |:| : : | || : |:| : | || 249 TPPAVLASALLDSGRHLES---VQALVRLVCQDPVHGDQNQATVRRWIEEWQPRCKAAAQ 305
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                          ---RPTWDPDYEIFDPSRSAIRMANWYALKDPRQ 79
                                                                                                                                                                                                                                                                          30 TEYELYTVGQQSTPDEWLHVDWPLRFDDGRAPWEEE-----SSAVRTSEWSAYRDPHQ 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAVAMLTAFMPE--WHTESNRWIDAVVKTMAAE---SDDNRALLARWIRDWSARAEAA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shinshi H, Wenzler H, Hofsteenge J, Ryals J, Sperisen C; WPI; 90-03117/05.
N-PSDB: Q03255, Q03256.
Recombinant DNA encoding beta-1,3-glucanase polypeptide(s) - useful in plant protection and biomass conversion pref. isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beta-1,3-glucanase from cDNA clones pBSGluc39.1 and pBSGluc39.3.
Beta-1,3-glucanase; papermaking; polysaccharide hydrolase;
                                                                                                                                                                                                            59;
                                                                                                                                                                          Length 343;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                        Pred. No. 4.7e-11;
; Mismatches 145;
                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                           LWORPYVSTCNQDQQAL------ARLVPVLTMGSAA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 -LAPVAARALQDAGRAALDEVREQFHARAARLGIAL 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFLPTFSDCGIDAKESANALSRALANORAAVEGAGI 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .3z
/label=prepro leader peptide.
33. .370
                                                                                                                                                                        Score 178.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R03056 standard; protein; 370 AA.
                                                                                                                                                                                                        55;
                                                                                                                                                                                                                                          31 TRYOEGMMGAO -- POENFHY ----
                                                                                                                                                                     10.4%;
22.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -Jul-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression.
370 AA;
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-1989; 810555.
29-JUL-1988; US-353312.
(CIBA) Ciba Geigy AG.
                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from tobacco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana sp.
                                                                                                                                                                                                      17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JAN-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP-353191-A
                                                                                                                     Sequence
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R03056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 185
                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                             132
                                                                                                                                                                                                                                                                                                                                                                                                               129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R03056
   8888888888
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                                                                                                                                                                                                                                                                        a
                                                                                                                                                                                                                                                                                                           Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                           QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qq
                                                                                                                                                                                                                                                                                                                                                                             Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
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DB 1; Length 370;

No. 0.4;

Score 86.5; Pred. No. 0.4

5.0%;

Best Local Similarity

Query Match

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14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIG. M. OURSEND M. SCRULEID M. TOTT AH;

WPI: 97-192888/17.

Localised variation of colour density in the surface of a dyed

rellulosic rabric - uses cellulase compsn. able to hydrolyse

pritrophenyl -beta-1,4-cellobioside

Sisclosure; Pages 15-7; 23pp; English.

Che present sequence is the corrected version of the incorrect

Bacillus lautus (NCIMB 40250) endoglucenase Endo 3A described in

WO9110732. Endo 3 can be used in novel method of forming localised

colour density variation on the surface of a dyed cellulosic

fabric. The method comprises agitating the fabric in an aqueous

medium (PH 6.5 to 9.0) containing a family 5 cellulose,

e.g. the present sequence, which can hydrolyse p-nitrophenyl-beta

1.4-cellobioside, or a family 7 cellulase, and a mechanical

abrading agent or cellulose having abrading activity Each

cellulase displays 30 % or more of its maximum activity at pH 7.

"The process is useful to provide a stone washed look to blue jeans
                                                                                                                                                                                                                                                249
   Gaps
                                58 IFDPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVA 117
                                                                                                         -----YGTVFTAPAMFHAM 159
                                                                                                                                       ----HIASGMEHARWWYQKNVKDFWPDVKIKYIAVGNEISPVTGTSYLTSFLTPAMVNIY 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKAFFQEMATLYGNTPNVIYEIANEPNGNVSWADVKSYAEEVITAIRAIDPDGVVIVGSP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----VELFIAQNLALDGLLYPL----VYDRFVDERI--ALEGGSAVAMLTAFMPEWHT 258
                                                                      94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WGANMNNAQICALGYGTVFTAPAM-----FHAMDNLGVAQYLTRLALAMAEPDVLEAA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                --SNIEV-----MLGLPNSDVK
                                                                                                                                                                                                                                             VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML
                                                                                                                                                                                                                                                                   211 YPYFSYSGNPGQISLPYSLFTAPNVVQDGSRQYRNLFDAMLDSYYAALERSGGASVGIV
                                                                                                                                                                      160 DNLGVAQYLTRLALAMAEPDVL----EAAKATWTRDAAW--QPLRRYVEDT----LV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----WADP
     83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endoglucanase; Endo 3A; formation; localised; variation:
colour density; surface; dye; fabric; family 5; cellulose;
hydrolysation; p-nitrophenyl-beta-1,4-cellobioside; stone wash;
blue jeans; back staining.
Bacillus lautus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-NOV-1997 (first entry)
Corrected Bacillus Lautus (NCIMB 40250) endoglucanase Endo 3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 551;
     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -------WQPLRRYVEDTL------
   71;
                                                                                                       ----NAQICALG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.82;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 0.82
42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toft AH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.0%; Score 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                      W18790 standard; protein; 551 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Onishi M, Schulein M,
 35;
                                                                   LYDPNHGALQ----ALKG----
                                                                                                   118 ARALDVLVPLRHAAWGANMN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.68;
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NOVO ) NOVO-NORDISK AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-SEP-1996; DK0364.
08-SEP-1995; DK-000993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     staining.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 KATWTRDAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     551 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     without back
53;
                                                                                                                                                                                                                                                                                                                                                271 VS 272
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                                                                                                                                                                                                                                                                                                                250 TA 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fich M,
                                                                                                                                                                                                          151
                                                                   99
                                                                                                                                      95
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 Matches
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Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNLGVAQYLTRLALAMAEPDVL----EAAKATWTRDAAW--QPLRRYVEDT----LV-- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200 YPYFSYSGNPGQISLPYSLFTAPNVVVQDGSRQYRNLFDAMEDSYYAALERSGGASVGIV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 ARALDVLVPLRHAAWGANMN------NAQICALG------YGTVFTAPAMFHAM 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 HSASG----MEHARWWVQKNVKDFWPDVKIKYIAVGNEISPVTGTSYLTSFLTPAMVNIY 139
-ESNRWIDAVVKTMAAESDDNRALLARWTRDWS----ARAEAALAPVAA 302
                                                        ---NARKISWV-NWSLADKVETSAALMPGAS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 IFDPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---SNIEV-----MLGLPNSDVK 83
                                                                                                                                                                                                                                                                                                                                                                              inducible pathogenesis-related protein from infected plants. Example 32; page 46; 77pp; English.
This is the sequence of the plant pathogenesis-related protein (PRP), beta-1,3-glucanase. It confers systemic acquired resis-
                                                                                                                                                                                                                                                                                                                                                                                                                          tance to plants. The corresp. DNA is used, in a chimeric construct, to produce transpent plant cells or -tissues with the ability to regenerate into plants which are disease resistant. See also Q06179-86, Q06199-Q06207 and Q06829.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 359;
                                                                                                                                                                                                                                                                                                                                                                   Disease-resistant transgenic plants - obtd. using encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71; Indels
                                                                                                                                                                                                                                                          1.7-(1.1990): 105336.
24-MAR-1999): 105336.
24-MAR-1999): US-329918.
20-UNN-1989): US-368672.
20-OCT-1989): US-45504.
(CIBA ) CIBA GEIGY AG.
Ryals JA, Alexander DC, Goodman RM, Meins F, Payne GB; Stinson JR, Neuhaus J-M, Moyer MB; N-FSDB; Q06208.
                                                                                                                                                                                            Beta-1,3-glucanase plant pathogenesis-related protein.
Transgenic plants; disease resistance; chimeric DNA;
plant pathogenesis-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.0%; Score 85.5; DB 22.3%; Pred. No. 0.48; tive 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W27608 standard; Protein; 337 AA. W27608;
                                                                                                                                                              ΑĄ
                                                                               -----RALQDAGRAALDEVRE 318
                                                                                                     275 PTGGWTDAQLSESGKWVRDQIRQ 297
                                                                                                                                                            R07315 standard; protein; 359
                                                        SDASGNGGPYFPQSKEWIDFL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::||: |::
55 LYDPNHGALO----ALKG---
                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                            synthetic.
EP-392225-A.
17-OCT-1990.
                                                                                                                                                                                 31-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 TA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 3
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                                                        227
                                                                              303
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                                  259
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ID W2
AC W2
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                                                                                                                                     RESULT
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           g
                                  δλ
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14;
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 5; 46pp; English.

This is PR-glucanase of the tomato plant, and it has areas of complementarity to the ribbzyme coding region. The DNA sequence, (or homologue), encoding this protein, (or homologue), operably linked to a promoter or other regulatory sequence (providing suitable tissue and/or temporal specific expression), can be used to prepare a male sterile transgenic tomato plant. The male sterile tomato plants can be used to produce hybrid seeds. The DNA sequence of PR-glucanase can be used to restore male fertility to sterile plants containing gluconases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beta-1,3-glucanase from cDNA clones pCL28, pCL30, pCL31, pCL43 and pCL36.
Beta-1,3-glucanase; papermaking; polysaccharide hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----NAQICALG-----YGTVFTAPAMFHAM 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 IFDPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVA 117
                                                                                                                                                                                                                                                                                                                    Use of glucanase DNA to prepare male sterile transgenic tomato plant - and complementary sequences for restoring fertility, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               200 YPYFSYSGNPGQISLPYSLFTAPNVVVQDGSRQYRNLFDAMLDSVYAALERSGGASVGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 LYDPNHGALQ----ALKG-----ALKG------MLGLPNSDVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----HIASGMEHARWWVQKNVKDFWPDVKIKYIAVGNEISPVTGTSYLTSFLIPAMVNIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 DNLGVAQYLTRLALAMAEPDVL----EAAKATWTRDAAW--QPLRRYVEDT----LV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CIBA) Ciba Geigy AG.
Shinshi H, Wenzler H, Hofsteenge J, Ryals J, Sperisen C;
WPI; 90-031717/05.
N-PSDB; Q03249, Q03250, Q03251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 84.5; DB 1;
Pred. No. 0.56;
5; Mismatches 71;
                                                    PR-glucanase; transgenic plants; male sterility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=prepro leader peptide.
22. .359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R03054 standard; protein; 359 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.9%; Scoi
21.9%; Pred
tive 35; J
                                                                                                                                                                                                                 LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-JUL-1990 (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 ARALDVLVPLRHAAWGANMN-
                                                                                                                                                                                                                                         Scott RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                     11-APR-1996; GB-007517.
(GENE-) GENE SHEARS PTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUL-1989; 810555.
29-JUL-1988; US-353312.
                                                                                                                                                                                                                                                                                                                                                                        hybrid seed production
                                                                             Lycopersicon species WO9738116-Al.
                           romato PR-glucanase.
                                                                                                                              16-OCT-1997.
10-APR-1997; G00992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                               WPI; 97-512728/47.
N-PSDB; T73604.
                                                                                                                                                                                                                                         Perez P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP-353191-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 VS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
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                                                                                                                                                                                                                                         Paul W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R03054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
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                                                                                                                                                                    14;
                                                       as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beta-1,3-glucanase is involved in plant defence against pathogens and as it hydrolyses polysaccharides, useful in biomass conversion or paper making. The clones allow for transfer of the gene to other species and control of gene expression.
                   from tobacco.
Disclosure; Fig 4-6; 41pp; English.
Disclosure; Fig 4-6; 41pp; English.
Beta-1, 3-glucanase is involved in plant defence against pathogens and a it hydrolyses polysaccharides, useful in biomass conversion or paper making. The clones allow for transfer of the gene to other species and sequence 359 AA;
                                                                                                                                                                                                                                                            : : || | | | | : | | | : | : | ----HIASGMEHARWWVQKNVKDFWPDVKIKYIAVGNEISPVTGTSYLTSFLTPAMVNIY 139
                                                                                                                                                                                                                                                                                                              140 KAIGBAGLGNNIKVSTSVDMTLIGNSYPPSQGSFRNDARWFTDPIVGFLRDTRAPLLVNI 199
                                                                                                                                                                                                                                                                                                                                             -VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML 249
                                                                                                                                                                                                                                                                                                                                                               200 YPYFSYSGNPGQISLPYSLFTAPNVVVQDGSRQYRNLFDAMLDSVYAALERSGGASYGIV 259
                                                                                                                                                                                        58 IFDPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVA 117
                                                                                                                                                                                                                                          ----NAQICALG------YGTVFTAPAMFHAM 159
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                 Beta-1,3-glucanase derived from cDNA clones pGL28, pGL30 and pGL31.
Beta-1,3-glucanase; papermaking; polysaccharide hydrolase;
                                                                                                                                                                                                                                                                                             DNLGVAQYLTRLALAMAEPDVL----EAAKATWIRDAAW--QPLRRYVEDT----LV--
 Recombinant DNA encoding beta-1,3-glucanase polypeptide(s) - useful in plant protection and biomass conversion pref. isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant DNA encoding beta-1,3-glucanase polypeptide(s) - useful in plant protection and biomass conversion pref. isolated
                                                                                                                                                                    83;
                                                                                                                                          DB 1; Length 359;
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-JUL-1989; 810555.
29-JUL-1988; US-353312.
(CIBA) Ciba Geigy AG.
Shinshi H, Wenzler H, Hofsteenge J, Ryals J, Sperisen N-PSDB; Q03252.
                                                                                                                                                                  71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .21
/label=prepro leader peptide.
22. .359
                                                                                                                                      4.9%; Score 84.5; DB
21.9%; Pred. No. 0.62;
Live 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from tobacco.
Disclosure; Fig 7; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R03055 standard; protein; 359
                                                                                                                                                                                                                                          118 ARALDVLVPLRHAAWGANMN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-JUL-1990 (first entry)
                                                                                                                                                                   Conservative
                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicotiana sp
                                                                                                                                                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP-353191-A
                                                                                                                                                                                                                                                                                                                                                                                                                      260 VS 261
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                                                                                                                                                                                                                                                                                                                                                                                             TA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                         Query Match
                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R03055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                              Matches
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Gaps

Indels

71; DB 1;

4.9%; Score 84.5; DB 21.9%; Pred. No. 0.62; tive 35; Mismatches

Conservative

Local Similarity nes 53; Conserv

Matches

á

Query Match

Length 359;

58 IFDPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVA 117

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14;
                                                                                                                                                                                                                                                                     200 YPYFSYSGNPGQISLPYSLFTAPNVVVQDGSRQYRNLFDAMLDSVYAALERSGGASVGIV 259
                                                                                                         ----HIASGMEHARWWVQKNVKDFWPDVKIKYIAVGNEISPVTGTSYLTSFLTPAMVNIY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 YPYFSYSGNPGQISLPYSLFTAPNVVVQDGSRQYRNLFDAMLDSVYAALERSGGASVGIV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----YGTVFTAPAMFHAM 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----HIASGMEHARWWVQKNVKDFWPDVKIKYIAVGNEISPVTGTSYLTSFLTPAMVNIY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 IFDPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVA 117
                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 LYDPNHGALQ-----ALKG-------SNIEV-----MLGLPNSDVK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The amino acid sequence codes for the basic beta-1,3-glucanase from N.tabacum, it is truncated at the 5' end and does not comprise the entire signal peptide which is necessary to ensure that the beta-1, 3-glucanase is properly targetted to the central vacuole in transgenic plants. The enzyme acts to degrade the cell membranes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plant pathogens and can be used in conjunction with one or more hydrolytic enzymes to improve its anti-pathogenic action. See also
  ----YGTVFTAPAMFHAM
                                                                                                                                                  160 DNLGVAQYLTRLALAMAEPDVL----EAAKATWTRDAAW--QPLRRYVEDT----LV--
                                                                                                                                                                                                                                            -------VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNLGVAQYLTRLALAMAEPDVL----EAAKATWTRDAAW--QPLRRYVEDT----LV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - comprise lytic peptide(s) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----NAQICALG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.9%; Score 84.5; DB
21.9%; Pred. No. 0.62;
iive 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PA, Garcia-Olmedo
                                                                  ----NAQICALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-pathógen; transgenic plant; pGLN17.
Nicotiana tabacum.
EP-448511-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Page 29; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R14028 standard; Protein; 359
                                                              118 ARALDVLVPLRHAAWGANMN-
::||: |:: |||
55 LYDPNHGALQ----ALKG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ryals JA, Gay PB, Ahl Goy
WPI; 91-283478/39.
N-PSDB; Q13750.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-pathogenic compsns.
hydrolytic enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-1991.
04-MAR-1991; 810144.
12-MAR-1990; US-491801.
(CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-1, 3-glucanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                          261
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Best Local Simi
Matches 53;
                                                                                                                                                                                                                                                                                                                               250 TA 251
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                                                                                                                                                                                                                                                                                                                                                                          260 VS
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                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                         84
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DNA encoding pathogenesis-related glucanase proteins - useful for producing transgenic plants with enhanced disease or pest resistance Disclosure; Column 247-248; 169pp; English.

The present invention describes a DNA molecule encoding a pathogenesis-related (PR) protein having beta-1,3-glucanase activity selected from PR-2, PR-2', PR-N', PR-N' pr-O and PR-O'. Also described are; (i) a chimeric gene comprising the above DNA molecule linked to a heterologous promoter; (ii) a vector containing the chimeric gene; (iii) a host cell containing the chimeric gene; (iv) a transgenic plant (iii) a host cell containing the chimeric gene; (iv) a transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    containing the chimeric gene; and (v) a seed from the transgenic plant. The DNA molecule is used to produce transgenic plants with enhanced disease or pest resistance. The present sequence represents a tobacco beta-1,3 glucanase protein for plasmid pGLN17 from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 ARALDVLVPLRHAAWGANMN-----NAQICALG------YGTVFTAPAMFHAM 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 YPYFSYSGNPGQISLPYSLFTAPNVVVQDGSRQYRNLFDAMLDSVYAALERSGGASVGIV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 IFDPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----HIASGMEHARWWVQKNVKDFWPDVKIKYIAVGNEISPVTGTSYLTSFLTPAMVNIY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tobacco beta-1,3-glucanase protein clone pGLN17.
Chemically regulatable DNA promoter; expression control; pesticide;
herbicide tolerance; beta-1,3-glucanase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 DNLGVAQYLTRLALAMAEPDVL----EAAKATWTRDAAW--QPLRRYVEDT----LV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.9%; Score 84.5; DB 1; Length 359; 21.9%; Pred. No. 0.62; ive 35; Mismatches 71; Indels 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                              Moyer MB, Payne GB, Ryals JA, Ward ER;
WPI; 99-059180/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W73543 standard; Protein; 359 AA.
W73543;
                                                                                                                                                                                                                                                                                                           16-JUL-1993; US-093301.
13-JAN-1994; US-181271.
(NOVS ) NOVARTIS FINANCE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-1995; 456262.
31-MAY-1995; US-456262.
(NOVS ) NOVARTIS FINANCE CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                US-768122.
US-848506.
US-973197.
                                                  US-425504.
US-580431.
US-632441.
                                                                                                                                                                                                                                                      US-042847.
US-045957.
US-329018
                                                                                                                                     US-678378
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US5851766-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; V81609
                                                                                07-SEP-1990;
21-DEC-1990;
                                                                                                                                     01-APR-1991;
                                                                                                                                                                      27-SEP-1991;
                                                                                                                                                                                             06-MAR-1992;
                                                                                                                                                                                                                              06-NOV-1992;
                                                                                                                                                                                                                                                         06-APR-1993;
                                                                                                                                                                                                                                                                                12-APR-1993;
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Best Local Simil
Matches 53; (
                                                     20-0CT-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 ----HIASGMEHARWWVQKNVKDFWPDVKIKYIAVGNEISPVTGTSYLTSFLTPAMVNIY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 DNLGVAQYLTRLALAMAEPDVL----EAAKAŢWTRDAAW--QPLRRYVEDT----LV-- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 YPYFSYSGNPGQISLPYSLFTAPNVVVQDGSRQYRNLFDAMLDSVYAALERSGGASVGIV 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Beta-1,3-glucanase protein for plasmid pGLN17.
Regulation; transcription; plant tissue; chimeric construction; PR; pathogenesis-related protein; anti-pathogenic; transgenic plant; beta-1,3-glucanase activity; pest resistance.
Nicotiana sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 LYDPNHGALQ-----ALKG------ALKG------SNIEV-----MLGLPNSDVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.9%; Score 84.5; DB 1; Length 359; Best Local Similarity 21.9%; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Mismatches
                                                                                                                                                                   03-JUL-1992 (first entry)
Protein encoded by plasmid pGLN17 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W83440 standard; Protein; 359 AA.
                                                                                                             R22005 standard; Protein; 359 AA
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08-DEC-1998.
31-MAY-1995, US-457364.
31-MAY-1995, US-457364.
08-MAR-1988; US-155667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also 0022158-72.
                                                                                                                                                                                                                           Beta 1,3-glucanase.
                                                                                                                                                                                                                                                         Nicotiana tabacum.
EP-474601-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to pathogens
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14;

Gaps

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For chemically controlling expression in transformed plants

Disclosure, Column 191-194, 175pp, Engglish.

Corremically controlling expression in transformed plants

Disclosure, Column 191-194, 175pp, Engglish.

Corremically controlling expression in transformed plants

Correct The gene can be isolated using the method of the invention.

Correction is for isolating a chemically regulatable DNA promoter

Correction regulated a chemically regulatable DNA promoter

a plant tissue. The method allows isolation of sequences which will be

Correcting regulatable sequence. This is useful in plants with a

con-coding regulator, the regulator being applied before or with the

correction or pesticide detoxification mechanism under the control of a

herbicide or pesticide detoxification mechanism under the control of a

confermical regulator, the regulator being applied before or with the

correction or pesticide to give optimal tolerance. The promoter fragment

beight, shape, development, male or female sterility, and the ability

correction of the promoter allows the regulation of production of

the plant to withstand cold, heat, salt and drought. The chanical

compounds, e.g. flavours, fragrances, pigments, natural sweeteners,

conflowerinal feedstocks, antimicrobials and pharmaceuticals, by

conflowerinal feedstocks, antimicrobials and pharmaceuticals, by

conflowerinal feedstocks, antimicrobials and pharmaceuticals, by

conditions of free expression either throughout the whole plant, or in

conflowering the leaves with the chemical regulator. Controlling the

conflowering the leaves with the chemical copialating chemical in

conflowering the leaves with the chemical regulator. Controlling the

control of the production of cultivated crops allows processes such

control of the production of cultivated crops allows processes such

control of the production of cultivated crops allows processes such

control of the production of cultivated crops allows processes such
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----SNIEV----MLGLPNSDVK 83
                                                                             regulatable DNA sequences in plants - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    140 KAIGEAGLGNNIKVSTSVDMTLIGNSYPPSQGSFRNDARWFVDPIVGFIRDTRAPLLVNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 YPYFSYSGNPGQISLPYSLFTAPNVVVQDGSRQYRNLFDAMLDSVYAALERSGGASVGIV
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A protein with stereoselective transaminase activity.
Stereoselective: transaminase activity; optically active amine; R-chirality; ketone; synthetic intermediate; pharmaceutical; agrochemical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.9%; Score 84.5; DB 1; Length 359; 21.9%; Pred. No. 0.62; ive 35; Mismatches 71; Indels 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71; Indels
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Best Local Similarity 21.99
Watches 53; Conservative
                                                                      Isolating chemically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------VFTAPAMF------HAMDNLGVAQYLTRLALAMAEPDVLEAAKA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 A------EGSGFNVVVIKDGVVRS-PGRAALPGITRKTVLEIAESLGHEAILADI 262
                                                                                                                                         Production of optically active amine(s) from ketone(s) and an amino donor using a transaminase derived from an Arthrobacter species. Claim 22: Page 56-57: 84pp; Japanese.
The present sequence represents a protein with stereoselective transaminase activity. The transaminase is used to produce the optically active amines (having R-chirality) of the invention. A ketone is treated with a transaminase in the presence of a primary amine as amino donor to produce the amines. The chiral amines are synthetic intermediates for use as pharmaceuticals and agrochemicals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 DYEL-DPANPLAGGAAWIEGAFVPPSEARISIFDQGYLHSDVTYTVFHVWNGNAFRLDDH 78
                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 RDITKHRPQVYMYAVPYQWIVPFDRIRDGVHAM----VAQSVRRTPRSSIDPQV-----
                                                                                                                                                                                                                                                                                                                                                                                     Score 84; DB 1; Length 325;
Pred. No. 0.6;
2; Mismatches 100; Indels 116;
                                                                   Hasegawa J, Ikenaka Y, Iwasaki A, Kizaki N, Matsumoto K,
                                                                                                                                                                                                                                                                                                                                                                                     4.9%; Scc
21.5%; Pre
tive 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 DYEIFDPSRSAIRMANW----
                                                                                                                                                                                                                                                                                                                                                                                                                       68; Conservative
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                                     JP-121732.
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                                                    (KANF ) KANEKA CORP.
                20-APR-1998; J01814.
23-APR-1997; JP-1217
                                                                                          Ogura M, Yamada Y;
WPI; 98-583664/49.
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                            N-PSDB; V73146.
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Search completed: September 26, 2000, 20:11:41 Job time: 10365 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

September 26, 2000, 19:19:06; Search time 60.65 Seconds (without alignments) 83.660 Million cell updates/sec Run on:

US-09-430-029-3 Title:

1723 1 MTIELKTVDIKPĻRHTFAHV.....ALDEVREQFHARAARLGIAL 331 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

152396 seqs, 15329161 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_AA:\* Database :

/cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/pactfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 2. Appli	Patent No. 5171684	•	ω,	1	86		98	98	98	0	98	98'	98,	9	98	σ	98,	2,	4	4	4	3,	55,	2,	5,	'n	Sequence 3, Appli
SUMMARIES	ID	US-08-319-387-2		US-08-499-215-2	-08-756-	US-09-033-537A-1	П	449-315-9	4	9-043-	-456	5-416-9	US-08-455-244-98	US-08-454-876-98	US-08-457-364-98	US-08-456-262-98	US-08-456-240-98	US-08-455-736-98	US-08-971-217-98	US-08-471-119A-2	US-08-620-605D-4	US-09-005-232A-4	PCT-US95-11684-4	US-09-019-201A-3	US-08-282-197C-55	-08-206-0	-08-804-2	-08-895-	US-09-195-391-3
	DB																											7	
	Query Match Length	331	327	342	560	551	359	359	359	359	359	359	359	359	359	359	359	359		15281	437	464	1810	516	397	457	1611	694	694
ď	Query Match	74.4	10.8	10.4		٠	•		4.9	•	4.9	٠	•	4.9	4.9		4.9	4.9	4.9			4.8		4.6	4.5	•	4.5	4.5	4.5
	Score	1282	186	178.5	87	98	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84.5	84	82	œ	79.5	ω.	7.8	7.8	78	77	77
	Result No.	П	5	ю	4	Ω.	9	7	<b>&amp;</b>	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28

15, 10, 22, 12,	Sequence 1, Appli Sequence 1, Appli Sequence 38, Appl Sequence 50, Appl Sequence 50, Appl Sequence 14, Appl Sequence 14, Appl
US-08-047-413-15 US-08-229-050-15 US-08-804-227C-10 US-08-804-198-4 US-08-466-583-2 PCT-US95-07820-2 US-08-804-227C-2 US-08-81-237C-2 US-08-81-237-10 US-08-81-237-10	US-09-195-391-1 US-09-195-391-1 US-08-602-359A-38 US-08-254-021-50 US-08-618-446-50 US-08-804-227C-14 US-08-835-099A-9
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00000000000000000000000000000000000000	0 6 4 4 4 4 4 4 9 0 0 0 0 0 0 0 0 0 0 0 0 0

# ALIGNMENTS

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Sequence 2, Application US/08319387
Patent No. 5543317
GENERAL INFORMATION:
APPLICANT: Shields, Malcolm S.
APPLICANT: Francesconi, Stephen C.
TITLE OF INVENTION: Microbial Degradation of Trichloroethylene, TITLE OF INVENTION: Dichloroethylenes and Aromatic Pollutants NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,387
                                                                                                                                                                                                                                  ADDRESSEE: Saliwanchik & Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: US/US/SIS/SU/SIS/SU/SIS/SU/SIS/SIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/167,457
FILING DATE: 15-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,718
FILING DATE: 02-MAY-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UM
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I: 331 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 904-375-81(TELEFAX: 904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-08-319-387-2
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                                                                                                                                                                                                                                                                                                            STATE: FI COUNTRY:
US-08-319-387-2
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275 NPDNHAVIEGWIEKWRPLADRA 296
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                                                                                                                           APPLICANT: Saeki, Hisashi APPLICANT: Miura, Akira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-499-215-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                              GENERAL INFORMATION:
APPLICANT: Saeki,
                                                                                                                                                                                                                                                                                                    20037-3202
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-08-756-317-8
                                                 RESULT 3
US-08-499-215-2
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                                                                                                                                                                                                                                                                        EGGSAVAMITAFMPEWHTESNRWIDAVVKTWAAESDDNRALLARWTRDWSARAEAALAPV 300
                                                                                                                                                                                                                                                                                                                                   241 NGGSAVAMLTTFMPEWHDESSRWVDAVVKTMATESEDNKALL:HWLRTWEDQAASALLPV 300
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                                                                                                                                              LEAAKATWIRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGLLYPLVYDRFVDERIAL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 QFNEREHDQMVREGWEHTMARCYSPLRYLFHCLQMSSAYVQQMAPASTISNCCILQTADS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAMAEPDV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          102 FVESRRMIGLMRDDVAARALDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDN 161
                                 Gaps
                                                                                                                             61 PSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D--YEIFDPS------RSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFE 101
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                                                              1 MTIELKTVDIKPLRHTFAHVAQNIGGDKTATRYQEGMMGAQPQENFHYRPTWDPDYEIFD 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 IGVAQYLTRLA----LAMAEPD--VLEAAKATWTRDAAWQPLRRYVEDTLVVADPVELF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YEN, KWANG-MU; BLATT, LAWRENCE M.; KARL, MICHAEL R.
TITLE OF INVENTION: BIOCONVERSIONS CATALYZED BY THE TOULUENE
MONOOXYGEARSE OF PSEUDOMANS MENDOCINA KR-1
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/07/590,374
FILING DATE: 28-SEP-1990
PRIOR APPLICATION NUMBER: 117,631
FILING DATE: 05-APR-1988
 Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 327;
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                                 Indels
                                 57:
74.4%; Score 1282; DB 1; 72.9%; Pred. No. 2.9e-132; iive 32; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                  AARALQDAGRAALDEVREQFHARAARLGI 329
                                                                                                                                                                                                                                                                                                                                                                                                                 301 AEMALAENGHDALEEVROOLRAALRRPGL 329
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                Best_Local Similarity 72.9
Matches 240; Conservative
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;Patent No. 5171684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 WPFVEYGLFLSLAYAVRQAMSDTVQFSVVFQAVDRMRLLQDIVHHLDHLQESPEFSDAGA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248 TPPAVLASALLDSGRHLES---VQALVRLVCQDPVHGDQNQATVRRWIEEWQPRCKAAAQ 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---RHAA 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 KATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGLLYPLVYDRFVDERIALEG-G
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                                                                                                                                TITLE OF INVENTION: BIOLOGICAL DEGRADATIVE
TITLE OF INVENTION: TREATMENT OF CHLORINE-SUBSTITUTED ETHYLENE
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10.4%; Score 178.5; DB 1; Length 342; 22.9%; Pred. No. 1.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 FYYASWATTRARQQDAMESNFEFVESRRMIGIMRDDVAARALDVLVPL---
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas STREET: 2100 Pennsylvania Avenue
CITY: Naw.
STATE: Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SFLPTFSDCGIDAKESANALSRALANQRAAVEGAGI 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP Hei-6-179689
FILING DATE: 08-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, V SOFTWARE: & WordPerfect version 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/499,215 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
; Sequence 2, Application US/08499215; Patent No. 5612204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
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E: No. 59580830 No. 5958083disk of No. 5958083th America, Inc. 405 Lexington Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDASGNGGPYFPQSKEWIDFL------NARKISWV-NWSLADKVETSAALMPGAS 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78; Indels
                                                                  Sequence 1, Application US/09033537A

Patent No. 5958083

GENERAL INFORMATION:
APPLICANT: Onishi, Masahiro
APPLICANT: Fich, Merete
APPLICANT: Toft, Annette Hanne
APPLICANT: Sh Lein, Martin
TITLE OF INVENTION: Prevention Of Back-Staining
TITLE OF INVENTION: In Stone Washing
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.0%; Score 86; DB 18.6%; Pred. No. 0.49 tive 42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4492.204-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/033,537A FILING DATE: 02-MAR-1998 CLASSIFICATION: 008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/DK96/00364
FILING DATE: 03-SEP-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----RALQDAGRAALDEVRE 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Green, Reza
REGISTRATION NOMBER: 38,475
REFERENCE/DOCKET NUMBER: 445
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 KATWTRDAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0993
FILING DATE: 08-SEP-1995
APPLICATION NUMBER: PCT/I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 551 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-878-9655
                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                                                                                            CITY: New York STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 10174
                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY:
US-09-033-537A-1
                                                   US-09-033-537A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 RSAIRMANWYALKDPRQFYYASWATIRARQQDAMESNFEFVESRRMIGLMRDDVAARALD 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---TWTR--DAAWQPLRRYVEDILVVAD 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 LKTVDIKPLRHTFAHVAQNIGGDKTATRYQEGMMGAQPQENFHYRPTWDPDYEIFD--PS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 VLVPLRHAAWGA-NMNNAQICALGYGTVFTAPAMEH-----AMDNLGVAQYLTRL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVELFIA----QNLALDGLLYPLVYDRFVDERI----ALE-GGSAVAMLTAFMPEWHTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.0%; Score 87; DB 2; Length 560;
21.8%; Pred. No. 0.39;
Live 43; Mismatches 120; Indels 106;
                                                                                                                                              TITLE OF INVENTION: Improved Rhodospirillum Rubrum TITLE OF INVENTION: Poly-B-Hydroxyalkonoate Synthase CORRESPONDENCE: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        450 ITDHITPW-DAVXRSALLLGGQRRFILSN----SGHIQSILNP 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILING DATE: US/08/756,317
FILING DATE: 25-NOV-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                  ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,693
FILING DATE: 29-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: MOBT:008
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 8, Application US/08756317
Patent No. 5849894
GENERAL INFORMATION:
APPLICANT: Clemente, Thomas E.
APPLICANT: Kishore, Genesh M.
APPLICANT: Misky, Timothy A.
APPLICANT: Stark, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Patterson, Melinda L. REGISTRATION NUMBER: 33,062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33,062
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TELEFAX: (713) 787-1440
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 560 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-08-756-317-8
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 77210-4433
                                                                                                                                                                                                                                       ALL...
STREET: P.C.
TTTY: Houston
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APPLICANT: UKnes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Walliams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/08/181,271A
CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-70L-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
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FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                              Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               Sequence 98, Application US/08181271A
Patent No. 5614395
275 PTGGWTDAQLSESGKWVRDQIRQ 297
                                                                                                                                                                                                                        Alexander, Danny C.
Beck, James J.
Duesing, John H.
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Stinson, Jeffrey R.
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Neuhaus, Jean-Marc
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APPLICATION NUMBER: I
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COUNTRY: USA
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                                                                           RESULT 6
US-08-181-271A-98
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----NAQICALG------YGTVFTAPAMFHAM 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 ----HIASGMEHARWWQKNVKDFWPDVKIKYIAVGNEISPVTGTSYLTSFLTPAMVNIY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 IEDPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 LYDPNHGALQ----ALKG-----ALKG------SNIEV-----MLGLPNSDVK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 DNLGVAQYLTRLALAMAEPDVL----EAAKATWTRDAAW--QPLRRYVEDT----LV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.9%; Score 84.5; DB 1; Length 359; 21.9%; Pred. No. 0.37; Live 35; Mismatches 71; Indels 8
                                                                                                                                                                                                                                                                                          S-19825/P1/CGC 1727
                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UNY-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1983
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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Patent No. 5650505
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Friedrich, Leslie B.
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Payne, George B.
Sperison, Christoph
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Alexander, Danny C.
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                                                                                                                                                                                                                                                   NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEG ID NO: 98: SEQUENCE CHARACTERISTICS: LENGTH: 359 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 ARALDVLVPLRHAAWGANMN-
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                                                                                                                                                                                                                                                                                                                                                  (919)541-8689
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Best Local Similarity 21.99
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
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APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727 TELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/181, 271
FILING DATE: 13-7AN-94
APPLICATION NUMBER: 0S 08/093, 301
FILING DATE: 16-UDL-1993
PRIOR APPLICATION NUMBER: US 07/937, 197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION NUMBER: US 07/937, 187
FILING DATE: 1-APPLICATION DATA:
APPLICATION NUMBER: US 07/678, 378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PELLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-0CT 1989
PRIOR APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
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PRIOR APPLICATION DATA:
APPLICATION APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/449,315
FILING DATE: 24-MAY-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36,129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 12-APR-1993
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REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                               New York
: USA
                                                                                                                                                                                                                          Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 24 CLASSIFICATION:
                                                                                                                                                                                                                                                                                             10532
                                                                                                                                                                                                                                               STATE: N
COUNTRY:
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CITY: Ha
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                                                                                                                                                                                                                                                                                             ----NAQICALG-----YGTVFTAPAMFHAM 159
                                                                                                                                                                                                                                                                                                                      84 ----HIASGMEHARWWVQKNVKDFWPDVKIKYIAVGNEISPVTGTSYLTSFLTPAMVNIY 139
                                                                                                                                                                                                                                                                                                                                                               ---EAAKATWTRDAAW--QPLRRYVEDT----LV-- 206
                                                                                                                                                                                                                                                                                                                                                                                    ------VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                   200 YPYESYSGNPGQISLPYSLFTAPNVVVQDGSRQYRNLFDAMLDSVYAALERSGGASVGIV 259
                                                                                                                                                                                        83; Gaps
                                                                                                                                                                                                                                                           ---SNIEV-----MEGLPNSDVK 83
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                                                                                                                                                    Length 359;
                                                                                                                                                                                        Indels
                                                                                                                                                                                      71;
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                                                                                                                                                    Score 84.5; DB 1;
Pred. No. 0.37;
                                                                                                                                                                                      35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIBA-GEIGY Corporation
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Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
Neuhaus, Jean-Marc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 98, Application US/08444803 Patent No. 5654414
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Sperison, Christoph
Stinson, Jeffrey R.
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APPLICANT: Alexander, Danny C.
APPLICANT: Beck, James J.
                                                                                                                                                   4.9%;
                                                                                                                                                                                                                                                                                                                                                             160 DNLGVAQYLTRLALAMAEPDVL--
                                                                                                                                                                                                                                                                                           118 ARALDVLVPLRHAAWGANMN---
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                                                                                                                                                                                                                                                         55 LYDPNHGALQ----ALKG---
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              SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acid
TYPE: amino acid
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                                                                                                                                                                                      53; Conservative
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APPLICATION NUMBER: US
INFORMATION FOR SEQ ID NO:
                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-315-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CH
TITLE OF INVENTION: DN
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                    Query Match
Best Local Similarity
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CITY: Hawthorne
STATE: New York
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APPLICANT:
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160 DNLGVAQYLTRLALAMAEPDVL----EAAKATWTRDAAW--QPLRRYVEDT----LV-- 206
                                                                                                                     200 YPYFSYSGNPGQISLPYSLFTAPNVVVQDGSRQYRNLFDAMIDSVYAALERSGGASVGIV 259
                                                                                            -------VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CHELICATION NUMBER: US/08/449,043
FILING DATE: 24-MAY-1995
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PRIOR APPLICATION DATA:
FILTNA
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PRIOR APPLICATION NUMBER: US 07/305,566
FTI.ING DATE: 6-FEB-1989
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FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                      Sequence 98, Application US/08449043
Patent No. 5689044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Duesing, John H.
Friedrich, Leslie B.
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Stinson, Jeffrey R.
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Alexander, Danny C.
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Payne, George B.
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Harms, Christian
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Ward, Eric R.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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                                                                                                                                                                                                                                                                                                                       Patent No. 5689044
GENERAL INFORMATION:
APPLICANT: Ryals,
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S-19825/P1/CGC 1727
                                                                                                                                                                                            FILING DATE: 1-APR-1991
PRIOR APPLICATION DATE: APPLICATION DATE: APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/165.667
FILING DATE: FILING DATA:
                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 1-DEC-1990
PRIOR APPLICATION DATA:
                                                                                                                                             APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/425,504 FILING DATE: 20-0CT 1989 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
FAROR APPLICATION DATE: APPLICATION NUMBER: US 07/368,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/368,672 FILING DATE: 20-JUN-1989
                                                                                    16-JUL-1993
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                                                      08/181,271
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REFERENCE/DOCKET UNBER: S-TELECOMMUNICATION INFORMATION: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 24 MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 98:
19-MAY-1995
N: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 27-SEP-1991 PRIOR APPLICATION DATA:
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REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            359 amino acids
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                                                                      FILING DATE: 13-JAN-94
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             CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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APPLICATION NUMBER:
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Matches 53; Conserv
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                                                                                                           FILING DATE:
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Ryals, John A.
Goodman, Robert M.
Stinson, Jeffrey R.
STRING CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
VENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,265A
FILING DATE: 31-MAY-95
CLASSIFICATION: 435
                                                                                                                             AUDRESSEE: CIBA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRICE APPLICATION: 43.9

PRICE APPLICATION NUMBER: US 08/181,271

FILING DATE: 13-UAN-1994

PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/093,301

FILING DATE: 16-UUL-1993

PRICE APPLICATION NUMBER: US 07/937,197

FILING DATE: 6-NOV-1992

PRICE APPLICATION NUMBER: US 07/678,378

FILING DATE: 1-APR-1991

PRICE APPLICATION NUMBER: US 07/678,378

FILING DATE: 6-FEB-1999

PRICE APPLICATION NUMBER: US 07/165,667

FILING DATE: 6-FEB-1989

PRICE APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988

PRICE APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988

PRICE APPLICATION NUMBER: US 07/165,667

FILING DATE: 8-MAR-1988

PRICE APPLICATION NUMBER: US 08/042,847
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DRC-1000
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PRIOR APPLICATION DATA:
APPLICATION
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APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/768,122 FILING DATE: 27-SEP-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/580,431 FILING DATE: 7-SEP-1990
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FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/425,504 FILING DATE: 20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 07/368,672
                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-1989
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 20-JUN-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
  APPLICANT: Ryals, John APPLICANT: Goodman, Robe APPLICANT: Goodman, Teff TITLE OF INVENTION: CHEMICALL OF INVENTION: DNA NUMBER OF SEQUENCES: LICORRESPONDENCE ADDRESSE: CIBA-GEIGY
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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Pred. No. 0.37;
5; Mismatches 71;
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PRING DATE: 27-SEP-1991
PRIOR APPLICATION DATE:
APPLICATION DATE:
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1989
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1989
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1983
                                                     FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION PARA:
                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                    APPLICATION NUMBER: US 07/425,504 FILING DATE: 20-OCT 1989
US 08/042,847
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 4.9%;
Best Local Similarity 21.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (919)541-8614
(919)541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 LYDPNHGALQ----ALKG---
                   FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US C
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                      160 DNLGVAQYLTRLALAMAEPDVL----EAAKATWTRDAAW--QPLRRYVEDT----LV-- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML 249
                                                                                                                                                                                                                                                                                                                                 118 ARALDVLVPLRHAAWGANMN-----NAQICALG------YGTVFTAPAMFHAM 159
                                                                                                                                                                                                                                                                                                                                                                  ----HIASGMEHARWWVQKNVKDFWPDVKIKYIAVGNEISPVTGTSYLTSFLTPAMVNIY 139
                                                                                                                                                                                                                                                        58 IFDPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVA 117
                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                            ---SNIEV-----MLGLPNSDVK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DIMES, SCOTT J.
APPLICANT: UNES, SCOTT J.
APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                       83;
                                                                                                                                                                                    Length 359;
                                                                                                                                                                                                                     71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                  DB 1;
                                                                                                                                                                                 Query Match 4.9%; Score 84.5; DB Best Local Similarity 21.9%; Pred. No. 0.37; Matches 53; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: CIBA-GEIGY Corporation 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 98, Application US/08455416 Patent No. 5777200
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Montoya, Alice
Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ryals, John A.
Alexander, Danny C.
Beck, James J.
Duesing, John H.
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Goodman, Robert M.
Harms, Christian
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Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuhaus, Jean-Marc
                 98:
                                                   : 359 amino acids
amino acid
                                                                                                                                                                                                                                                                                            55 LYDPNHGALQ ---- ALKG--
TELEFAX: (919)541-8689
               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                         ; MOLECULE TYPE: protein US-08-456-265A-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                            linear
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STREET: 7 Skylir
CITY: Hawthorne
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APPLICANT:
APPLICANT:
APPLICANT:
                                                                                          TOPOLOGY:
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US-08-455-416-98
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APPLICANT:
                                                     LENGIH:
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                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PADLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
FILING DATE: 24-MAR-1989
FILING DATE: 12-APR-1989
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1983
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION PURBER: US 07/165,667
FILING DATE: 8-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION AND APPLICATION DATA:
APPLICATION NUMBER: US/08/455,416
FILING DATE: 31-MAY-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
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APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
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APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-0CT 1989
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TELEPHONE: (919)541-8614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 98:
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REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (919)541-8689
                                                                                                            FILING DATE: 13-JAN-94 APPLICATION NUMBER: US
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                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
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Best Local Similarity
                                               CLASSIFICATION:
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----HIASGMEHARWWVQKNVKDFWPDVKIKYIAVGNEISPVIGTSYLTSFLTPAMVNIY 139
                                                                 140 KAIGEAGLGNNIKVSTSVDMTLIGNSYPPSQGSFRNDARWFVDPLYGFLRDIRAPLLVNI 199
                                                                                                         --VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML 249
                                                                                                                            200 YPYFSYSGNPGQISLFYSLFTAPNVVVQDGSRQYRNLFDAMLDSVYAALERSGGASVGIV 259
                                160 DNLGVAQYLTRLALAMAEPDVL----EAAKATWTRDAAW--QPLRRYVEDT----LV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10532
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DAFA:
APPLICATION NUMBER: US/08/455,244
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CIBA-GEIGY Corporation
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PRIOR APPLICATION DATA:
APPLICATION APPLICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/165,667 FILING DATE: 8-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                  Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, T., Frederick
Montoya, Alice
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Patent No. 5789214
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
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Stinson, Jeffrey R.
Uknes, Scott J.
Ward, Eric R.
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Neuhaus, Jean-Marc
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APPLICATION NUMBER: U
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APPLICANT:
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APPLICANT:
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APPLICANT:
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58 IFDPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVA 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : : || | | : | : || | 84 ----HIASGMEHARWWVQKNVKDFWPDVKIKYIAVGNEISPVTGTSYLTSFLTPAMVNIY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 KAIGEAGLGNNIKVSTSVDMTLIGNSYPPSQGSFRNDARWFVDPIVGFLRDTRAPLLVNI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 LYDPNHGALQ-----ALKG------SNIEV-----MLGLPNSDVK 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 DNLGVAQYLTRLALAMAEPDVL----EAAKATWTRDAAW--QPLRRYVEDT----LV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.9%; Score 84.5; DB 1; Length 359; 21.9%; Pred. No. 0.37; tive 35; Mismatches 71; Indels 8
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                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-5EP-1991
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 7-5EP-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
                                                                                                                 FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
                                                                                             US 07/632,441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-1
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 08
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                     PRIOR APPLICATION DATA:
                                                                                        APPLICATION NUMBER:
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Best Local Similarity
Matches 53; Conserva
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US-08-454-876-98
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FILING DATE: 20-JUN-1989
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: CLEA-GEIGY Corporation
STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
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PRICRATION TO STATE
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRICR APPLICATION DATE: US 07/937,197
FILING DATE: 6-NOV-1992
PRICR PAPLICATION NUMBER: US 07/937,197
FILING DATE: 1-NOV-1992
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 6-APR-1993
PRICHATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRICHAPLICATION DATE: US 07/632,441
FILING DATE: 21-DEC-1990
PRICHAPPLICATION NUMBER: US 07/425,504
FILING DATE: 20-0CT 1989
PRICHAPPLICATION NUMBER: US 07/425,504
FILING DATE: 20-0CT 1989
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION DATE: 1-APR-122.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, NCURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,876
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRICA DATE: 6-FEB-1989
PRIOR APPLICATION NAMES:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
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27-SEP-1991
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7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             Meins, Jr., Frederick
Montoya, Alice
                                                                               Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
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Sperison, Christoph
Stinson, Jeffrey R.
                        Alexander, Danny C.
Beck, James J.
Duesing, John H.
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Neuhaus, Jean-Marc
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Ward, Eric R.
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PRIOR APPLICATION DATA:
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CITY: Hawthorne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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ENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC FUNION: DNA SEQUENCES AND USES THEREOF
SQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
PRIOR DATE: 2000 1203
PRIOR PELLORION DATA: APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA: D8 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 21.9%; Pred. No. 0.37;
Matches 53; Conservative 35; Mismatches 71;
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Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
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Meins, Jr., Frederick
Montoya, Alice
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Sperison, Christoph
Stinson, Jeffrey R.
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                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
                                                                                                                                                                                                                          TELEPHONE: (919)541-8614
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
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55 LYDPNHGALQ----ALKG----
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Ward, Eric R.
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                                                                                                                                                                                                                                                                                                            : 359 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-454-876-98
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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APPLICANT:
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Page 11

14; 118 ARALDVLVPLRHAAWGANMN-----NAQICALG-----YGTVFTAPAMFHAM 159 84 ----HIASGMEHARWWVQKNVKDFWPDVKIKYIAVGNEISPVTGISYLTSFLTPAMVNIY 139 160 DNLGVAQYLITRLALAMAEPDVL----EAAKATWIRDAAW--QPLRRYVEDT----LV-- 206 207 ------VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML 249 58 IFDPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVA 117 200 YPYFSYSGNPGQISLPYSLFTAPNVVVQDGSRQYRNLFDAMLDSVYAALERSGGASVGIV 259 Gaps ---SNIEV-----MLGLPNSDVK 83 83; Williams, Shericca C.
VENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
VENTION: DNA SEQUENCES AND USES THEREOF
EQUENCES: 106 Length 359; 71; Indels SOFTWARE: Patentin Release #1.0, Version #1.25
CARRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,262
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435 Ouery Match 4.9%; Score 84.5; DB 2; Best Local Similarity 21.9%; Pred. No. 0.37; 35; Mismatches ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,301 Friedrich, Leslie B. Goodman, Robert M. Harms, Christian Meins, Jr., Frederick Montoya, Alice MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 98, Application US/08456262 Patent No. 5851766 GENERAL INFORMATION: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/181,271 Payne, George B. Sperison, Christoph Stinson, Jeffrey R. Ryals, John A. Alexander, Danny C. Moyer, Mary B. Neuhaus, Jean-Marc Duesing, John H. ::||: |:: ||| 55 LYDPNHGALQ----ALKG---Uknes, Scott J. Ward, Eric R. Beck, James J. 53; Conservative ZIP: 10532 COMPUTER READABLE FORM: CORRESPONDENCE ADDRESS: TITLE OF INVENTION: ITILE OF INVENTION: NUMBER OF SEQUENCES: CITY: Hawthorne STATE: New York US-08-457-364-98 US-08-456-262-98 260 VS 261 250 TA 251 APPLICANT: COUNTRY: APPLICANT: Matches Qγ qq δŏ qq δλ Db qq δ δž

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14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---VADPVELFIAQNLAL-DG-LLYPLVYDRFVDE-RIALE--GGSAVAML 249
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4.9%; Score 84.5; DB 2; Length 359;
Best Local Similarity 21.9%; Pred. No. 0.37;
Matches 53; Conservative 35; Mismatches 71; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
              PRIOR AND LAILS.

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-AFF-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,607
FILING DATE: 1-DEC-1990
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
PRIOR APPLICATION NUMBER: US 07/88,506
FILING DATE: 20-OCT 1989
PRIOR APPLICATION NUMBER: US 07/88,506
FILING DATE: 2-SEP-1991
PRIOR APPLICATION NUMBER: US 07/88,122
FILING DATE: 2-SEP-1991
PRIOR APPLICATION NUMBER: US 07/580,431
FILING DATE: 1-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 LYDPNHGALQ----ALKG---
16-JUL-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (919)541-8689 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08-456-262-98
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Db 200 YPYFSYSGNPGQISLPYSLFTAPNVVVQDGSRQYRNLFDAMLDSVYAALERSGGASVGIV 259
Qy 250 TA 251
Db 260 VS 261
Search completed: September 26, 2000, 20:22:37
Job time: 3811 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 26, 2000, 19:23:36; Search time 82.1 Seconds (without alignments) 249.499 Million cell updates/sec Run on:

US-09-430-029-3

1723 1 MIELKTVDIKPLRHTFAHV.....ALDEVREQFHARAARLGIAL 331 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

178050 segs, 61884766 residues Searched:

178050 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR\_64:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	2-	_		methane monooxygen	replication factor	replication factor	endoglucanase - Er	methane monooxygen	probable maltoolig	polyketide synthas	probable exonuclea	probable monoxygen	molybdopterin oxid	ATP-dependent Clp	4-hydroxybenzoate-	probable exonuclea	conserved hypothet	PopQ protein - Rhi		cellulase (EC 3.2.	pet112-like protei	probable RNA-direc	hypothetical prote	cal	⊣	poly(3-hydroxyalka	hypothetical prote	ical	probable monooxyge
SUMMAKIES	ŒĨ	B37831	S44304	4728	S15208	T18305	T18306	S39962	JL0101	G70763	T30226	T03465	G70932	C75525	G75442	A58538	B70898	A75412	S58233	672658	S54744	T45408	T00078	S01984	T35781	S36851	S29307	T10037	T04193	T46818
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æ	Query Match	5.	45.2	7.	٠		6.1	6.1	9.0	5.7	5.7	5.6	5,3	5.3	5,3	5.2	5.2	5.3	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.1	5.0	5.0	5.0	2.0
	Score	779.5	778.5	640.5	123	105.5	105.5	105	103	66	97.5	96	91.5	90.5		06	ъ.	89.5	ъ.	æ	ъ.	ъ.	8	•	7	7	87	87		86.5
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phenol 2-monooxygenase (EC 1.14.13.7) component L - Pseudomonas putida N;Alternate names: phenolhydroxylase chain B

299 PVAARALQDAGRAALDEVREQFHARAARLGI 329

QY

g

7

RESULT S44304

326

ABC transporter in	probable ATP-depen	peptide synthetase	ubiquinolcytochr	probable gatB - My	phosphoribosylamin	Ó-antigen biösynth	glucan endo-1,3-be	rep protein - Stre	hydroxyneurosporen	probable fadE6 pro	qlucan endo-1,3-be	1,3-beta-qlucanase	glucan endo-1,3-be	qlucan endo-1,3-be	endo-1,4-beta-xyla
F65254	E72611	T17483	JX0301	D70856	A81135	T18556	S12406	A31844	S32171	B70628	A30758	S13594	A39115	B39115	\$59634
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555	1273	3158	474	509	526	1275	369	456	485	731	359	365	370	370	909
5.0	5.0	5.0	5.0	2.0	5.0	5.0	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9	4.9
86.5	86.5	86.5	85.5	85.5	85.5	85.5	82	85	85	85	84.5	84.5	84.5	84.5	84.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	15
	7	.5 5.0 555 2 F65254 .5 5.0 1273 2 E72611	.5 5.0 555 2 F65254 .5 5.0 1273 2 E72611 .5 5.0 3158 3 I17483	.5 5.0 555 2 F65254 .5 5.0 1273 2 B72611 .5 5.0 3158 3 T17483 .5 5.0 474 2 JX0301	0 86.5 5.0 555 2 P65254 1 86.5 5.0 1273 2 B72611 2 86.5 5.0 3158 3 117483 3 85.5 5.0 474 2 3X0301 4 85.5 5.0 509 2 D70856	0 86.5 5.0 555 2 P65254 1 86.5 5.0 1273 2 B72611 2 86.5 5.0 3158 3 T17483 3 85.5 5.0 474 2 JX0301 4 85.5 5.0 509 2 D70856 5 85.5 5.0 526 2 A81135	0 86.5 5.0 555 2 P65254 1 86.5 5.0 1273 2 B72611 3 85.5 5.0 1378 3 E72611 4 85.5 5.0 474 2 JX0301 4 85.5 5.0 509 2 D70856 5 85.5 5.0 1275 2 T1855	0 86.5 5.0 555 2 P65254 2 86.5 5.0 1273 2 B72611 2 85.5 5.0 3158 3 T17483 4 85.5 5.0 474 2 JX0301 4 85.5 5.0 509 2 D70856 5 85.5 5.0 526 2 A81135 6 85.5 5.0 18556 7 85 4.9 369 2 S1246	86.5 5.0 555 2 F65254 86.5 5.0 1273 2 E72611 86.5 5.0 3158 3 117483 85.5 5.0 474 2 JX0301 85.5 5.0 509 2 D70856 85.5 5.0 1275 2 A81135 85.5 5.0 1275 2 118556 85 4.9 456 2 A31844	86.5 5.0 555 2 F65254 86.5 5.0 1273 2 E72611 86.5 5.0 1273 2 E72611 85.5 5.0 474 2 JX0301 85.5 5.0 509 2 D70856 85.5 5.0 526 2 A81135 85.5 5.0 1275 2 T1855 85.4 9 369 2 S12406 85 4.9 485 2 S321844	86.5 5.0 555 2 F65254 86.5 5.0 1273 2 E72611 86.5 5.0 1373 2 E72611 85.5 5.0 474 2 JX0301 85.5 5.0 509 2 D70856 85.5 5.0 1276 2 MR1135 85.5 5.0 1275 2 T18556 85 4.9 369 2 S12406 85 4.9 485 2 S32171 85 4.9 731 2 B70628	86.5 5.0 555 2 F65254 86.5 5.0 1273 2 E72611 86.5 5.0 1273 2 E72611 85.5 5.0 474 2 JX0301 85.5 5.0 509 2 D70856 85.5 5.0 1276 2 D70856 85.5 5.0 1275 2 T18556 85 4.9 456 2 A31844 85 4.9 485 2 S32171 85 4.9 359 2 A30528	86.5 5.0 555 2 F65254 86.5 5.0 1273 2 E72611 86.5 5.0 1273 2 E72611 85.5 5.0 474 2 JX0301 85.5 5.0 509 2 D70856 85.5 5.0 1275 2 A81135 85 4.9 369 2 S12406 85 4.9 456 2 A31844 85 4.9 731 2 B70628 84.5 4.9 731 2 B70628 84.5 4.9 365 2 S13594	86.5 5.0 555 2 F65254 86.5 5.0 1233 2 E72611 86.5 5.0 1233 2 E72611 85.5 5.0 474 2 JX0301 85.5 5.0 509 2 D70856 85.5 5.0 509 2 D70856 85.5 5.0 1275 2 H1855 85 4.9 456 2 A81135 85 4.9 456 2 A31844 85 4.9 731 2 B70628 84.5 4.9 359 2 A30758 84.5 4.9 359 2 A30758	86.5 5.0 555 2 F65254 86.5 5.0 1273 2 E72611 86.5 5.0 1273 2 E72611 85.5 5.0 474 2 JX0301 85.5 5.0 526 2 P70856 85.5 5.0 526 2 P70856 85.5 5.0 1275 2 T18556 85 4.9 456 2 A312406 85 4.9 485 2 S32171 84 5 4.9 359 2 S13594 84 5 4.9 370 2 A39115

# ALIGNMENTS

RESULT 1  Ba3781.  phenol 2-monooxygenase (EC 1.14.13.7) chain Pl - Pseudomonas sp. (strain CF600)  C;Species: Pseudomonas sp.  C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999  C;Accession: B37831  R;Nordlund, 1.; Powlowski, J.; Shingler, V.	J. Bacteriol. 172, 6826-6833, 1990 A;Title: Complete nucleotide sequence and polypeptide analysis of multicomponent phen A;Reference number: A37831; MUID:91072230 A;Reterence number: B37831 A;Accession: B37831 A;Status: preliminary A;Status: preliminary A;Residues: 1-331 < NOR>	A;Cross-references: GB:M60276; GB:M37764; NID:g151449; PIDN:AAA25940.1; PID:g151451 C;Superfamily: phenol 2-monooxygenase component L C;Keywords: oxidoreductase	Query Match Best Local Similarity 46.8%; Pred. No. 4.7e-59; Matches 155; Conservative 54; Mismatches 115; Indels 7; Gaps 4;	1 MTIELKTVDIKPLRHTFAHVAONIGGDKTATRYQEGMMGAQPQENFHYRPTWDFDYEIFD 60  :: :   :  :   : :::	61 PSRSAIRMANMYALKDPROFYYASWATTRARQODAMESNFEFVESRRMIGLMRDDVAARA 120 	121 IDVLVPERHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAMAEP 178 	179 DVLEAAKATWIRDAAWQPLRRYVEDTLVVADFVELFIAQNLALDGLLYPLYYDRFVDERI 238 :  :                          : : 180 EALDQAKAYWLDDPIWQGLRRYVEDSFVIRDWFELGLAQNLVLDGLLQPLMYQRF-DQWL 238	239 ALEGGSAVAMLTAFWPEWHTESNRWIDAVVKTWAAESDDNRALLARWIRDWSARAEAALA 298 
RESULT B37831 phenol 2 C; Specie C; Date: C; Access	J. Bacte A; Title: A; Refere A; Access A; Status A; Molecu	A;Cross: C;Superi C;Keywor	Query Best I Matche	Qy Db	Oy da	Oy 12 Db 12	Oy 17 Db 16	Qy 23 Db 23

Wed

EMBL Data Library, September 199

4;

Gaps

Indels

Length 333;

59

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A;Molecule type: DNA
A;Residues: 1-333 <EH2>
A;Cross-references: EMBL:236909; NID:9535279; PIDN:CAA85381.1; PID:9535281
A;Cross-references: EMBL:236909; NID:9535279; PIDN:CAA85381.1; PID:9535281
A;Experimental source: strain NCIB8250
A;Experimental source: strain NCIB8250
A;Octe: the nucleotide sequence was submitted to the EMBL Data Library, Seg C;Genetics: mopil
C;Superfamily: phenol 2-monooxygenase component L
C;Superfamily: phenol 2-monooxygenase component L
C;Keywords: aromatic hydrocarbon catabolism; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          239 VENGGRDIAILTEFMKDCLTDLAKWSDSVLKTAISESEDNKTLIQSWITELLPQVKQAFS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 PSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 I.DVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAM--AEP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 ALEGGSAVAMLTAFMPEWHTESNRWIDAVVKTMAAESDDNRALLARWTRDWSARAEAALA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTIELKTVDIKPLRHTFAHVAQNIGGDKTATRYQEGMMGAQPQENFHYRPTWDPDYEIFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            179 DVLEAAKATWIRDAAWQPLRRYVEDILVVADPVELFIAQNLALDGLLYPLVYDRFVDERI
                                                                                                                                                                                                                                                                                                   37.2%; Score 640.5; DB 1; 39.4%; Pred. No. 3.3e-47; iive 70; Mismatches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 AWAQTALTDSGIDSGLNKISER 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 PVAARALQDAG-RAALDEVREQ 319
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Best Local Similarity 22.3%;
Matches 74; Conservative 4
                                                                                                                                                                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 127; Conserva
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A;Molecule type: protein
A;Residues: 2-16 <FOX>
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                                                                                                                      A; Title: Cloning and sequences of the first eight genes of the chromosomally encoded (me A; Reference number: A58972; MUID:95129877
A; Reference number: A58972; MUID:95129877
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-331 < CALL
A; Cross-references: EMBL:X79063; NID:9483477; PIDN:CAA55661.1; PID:9483479
A; Reperimental source: strain P35X (NCBI 9869)
A; Rote: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
A; Reperimental source: strain P35X (NCBI 9869)
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1994
B; Herrmann, H; Mueller, C.; Schmidt, I.; Mahnke, J.; Petruschka, L.; Hahnke, K.
Mol. Gen. Genet. 247, 240-246, 1995
A; Title: Localization and organization of phenol degradation genes of Pseudomonas putida
A; Reference number: S54761; MUID:95272534
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 'MGIQQQEGTVD', 1-8, 'T', 10-57, 'R', 59-86, 'G', 88-331 < HEZ>
A; Cross-references: EMBL:880765; NID:9527546; PIDN:CAA56741.1; PID:9527548
A; Reperimental source: strain H
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
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547288
phenol 2-monocoxygenase (EC 1.14.13.7) chain mopL - Acinetobacter calcoaceticus
N.Alternate names: phenol hydroxylase
C.Species: Acinetobacter calcoaceticus
C.Species: Acinetobacter calcoaceticus
C.Species: Species: Acinetobacter calcoaceticus
C.Species: Solution and a sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C.Accession: S70081, 547288
R.Ehrt, S.: Schirmer, F.; Hillen, W.
Mol. Microbiol. 18, 13-20, 1995
A.Title: Genetic organization, nucleotide sequence and regulation of expression of calculation number: S70080; MUID:96154937
A.Reference number: S70081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
C;Species: Pseudomonas putida
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: C58975; S54767; S44304; S47415
Gene 151, 29-36, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 IDVLVPELRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAM--AEP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALEGGSAVAMLTAFMPEWHTESNRWIDAVVKTMAAESDDNRALLARWTRDWSARAEAALA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DVLEAAKATWIRDAAWQPLRRYYEDTLVVADPVELFIAQNLALDGLLYPLVYDRFVDERI
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46.8%; Pred. No. 5.7e-__,
*ive 54; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: phenol 2-monooxygenase component L
Keywords: oxidoreductase
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Matches 155; Conservative
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Best Local Similarity
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methane monooxygenase (EC 1.14.13.25) component A beta chain - Methylosinus trichospo N; Alternate names: methane monooxygenase hydroxylase beta chain C; Species: Methylosinus trichosporium C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Jun-1999 C; Accession: 515208; B39049; R; Cardy, D.L.N.; Laidler, V.; Salmond, G.P.C.; Murrell, J.C.
Mol. Microbiol. 5, 335-342, 1991
A; Title: Molecular analysis of the methane monooxygenase (MMO) gene cluster of Methyl A; Reference number: 515207; MUID: 91251762
A; Molecule type: DNA
A; References: EMBL: X55394; NID: 944613; PIDN: CAA39069.1; PID: 944615
A; Cross-references: EMBL: X55394; NID: 944613; PIDN: CAA39069.1; PID: 944615
A; Title: Complex formation between the protein components of methane monooxygenase fractions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 394;
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0.0054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 123; DB Fred. No. 0.00949; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 KTATRYQEGMMGAQPQ---
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Db 47 KPLSEVEGLSCYAQPNPDWIAGGLDWGDWTQKFHGGRPSWGNESTELRTTDWY 99  73 ALXDP-RQFYYASWATTRARQQDAMESNPEFVESRRMIG-LMRDDVAARALDVLVPLR 128  1	ctor C protein - Emericel ricella nidulans, Aspergi 18306. 159, 1997 mber: Z18873 18306 iminary; translated from e: DNA c: DNA 1092 <raf> nces: EMBL:U86620; NID:92 3; 38/1; 68/2 6.1%; Score</raf>
Db 337 DFVGLYAKVEKSRADRSRRLRGAAASSAI 366  RESULT 5 T18305 replication factor C like protein - Emericella nidulans C; Species: Emericella nidulans, Aspergillus nidulans C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C; Accession: T18305 R; Kafér, E; May, G. Gene 191, 155-159, 1997	ra -
A;Title: The uvsF gene region in Aspergillus nidulans codes for a protein with homology A;Reference number: 218873 A;Reference number: 218873 A;Reference number: 118305 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Rossreferences: EMBL:U86619; NID:g1840141; PID:g1840142; PIDN:AAB63523.1 C;Genetics: A;Gene: uvsF	123 816 178 876 231 916
Duery Match 6.1%; Score 105.5; DB 2; Length 1092; Best Local Similarity 20.2%; Pred. No. 0.62; Matches 69; Conservative 49; Mismatches 144; Indels 79; Ga 26 GDKTATRYGEMMGAQPOENFHYETHWDDVEIFDPESRAIRMANWYALKDPRQFY [	QY 286 TRDWSARAEAALAPVAARALQDGRAALDEVRE 318
AMIQENYIRTREPRANNYEGKERKIKLILELAWGANMNNAQICALGYGTVETAPAMEHAMDNIL	
DGKD,	Query Match 6.1%; Score 105; DB 2; Length 505; Best Local Similarity 23.2%; Pred. No. 0.25; Matches 68; Conservative 38; Mismatches 73; Indels 114; Gaps 17; Qy 112 MRDDVAARALDVLVPLRHAAWGANNNNAQICALGYGTVFTAPAMFHAMDNL 162 111

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5 F	163 GVAQYLTRLALAMAEPDVLEAAKATWTRDAAWQP 196		ARALQD
3 8	GVIIIIDMBILDOUDLYNIANGEVINNGQIRFFAEMAGLIGSSKNVIIEIANEFNGGVINNGQIRF	DD 330 A-ALKDFM	LKDFM
ž 6	19. YALEWIDILWANDYELETAQNE-ALDGLEYPLVEDKEVDEK 23/ 	RESULT 9	
δλ		probable maltoolige C; Species: Mycobact	cobact
qa	FVSEWGTSDASGNGGPFLPESQT	C, Accession: (	32076
QY	283 ARWTRDWSARAEAALAPVAARALQDAGRAALDEVREQFHARAARLG 328 	Connor, R.; Davie Rajandream, M.A.; I Nature 393, 537-54	Davie 1.A.; 1
RESULT JL0101	LT 8 01	A;Authors: Sq: A;Title: Decil A;Reference n: A;Accession: C	fares, pherinumber G7076
meth N;Al	ane monooxygenase (EC 1.14.13.25) A beta chain precursor - Methylococcus capsulatus ternate names: methane hydroxylase endes: Methylococcus canculating	A; Molecule type	liming
C, Da	te: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 15-Nov-1996 cession: JL0101	A; Cross-refere A; Experimental	ences
R;St Arch A;Ti	R:Stainthorpe, A.C.; Murrell, J.C.; Salmond, G.P.C.; Dalton, H.; Lees, V. Archim Microbiol. 152, 154-159, 1989 Archim Microbiol. 152, 154-159, 1989 Architle: Molecular analysis of methane monooxygenase from Methylococcus cansulatus (Pa+H	C;Genetics: A;Gene: glgZ	1 1
A; Re A; Ac	ference number: A90083; MUID:89373399 cession: JL0101		; ;
A; Mo A; Re	lecule type: DNA sidues: 1-387 <staa mmont: Met-1 is removed after translation</staa 	Query Match Best Local Simila	sh   Simila
300	manch: Not its removed after transfaction.  mment: Residues 2-41 were confirmed by direct protein sequencing.  mment: This enzyme is responsible for the initial oxygenation of methanel	7	ETEDP
atic C;Co	and heterocyclic compounds.		::::    PEFRVWAPI
C;Cc met	C;Comment: Protein A comprising three chains, alpha, beta and gamma, is a non-heme iron methane. Protein B is a single subunit regulatory protein containing no prosthetic group	QY 80 FYY	FYYASWAT
C; Ge	Voprocein responsible for the transfer of reducing equivalents from NADH to protein A. (Schedics:	Db 62	
A) G	oxidoreductase	QY 139 ADICALGY	CALGY
4	SoffFroduct: Methane MonooAyyenase A Deta Chain *Status predicted <mai></mai>	Db 98 AVI	AVIYELHIC
Qu	Query Match 6.0%; Score 103; DB 2; Length 387; Best Local Similarity 20 1%; Pred No 0 27.	Qy 199 RYVE	RYVEDTLV
Ma	vative 44; Mis	Db 134	
oy da	28 KTATRYGEGMMGAQPQENFH-YRPTWDPDYEIFDPSKSAIRMANWY 72	Qy 238 IALA	IALEGGSAV
6	ALKDPROFYYASWATTRARCODAMESNEREVESPRATGIMRDDVAARA: DVIRAA-	292	YEMHLGEDY -RAEAALAI
DP G		244	: I I
QY	132WGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTR 170	RESULT 10	
QY	LALAMAEPDVLEAAKATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGL	polyketide synthase C, Species: Strepton	reptor
qa	GFLAKIVPGFDESTAVPKAEWFNGEVYKSARLA	C, Accession: 1 R; Aparicio, J.	T30226
QY	225 17PLVYDRFVDERIALEGGSAVAMLTAFM 253 : :   :  :  :  :  :  :  :  :  :  :  :	<pre>Gene 169, 9-16, 199 A:Title: Organizati A:Reference number:</pre>	6, 199 nizati umber
QY		A; Accession: T30226 A; Status: prelimina	T30226
qq	295 VQDLYYNCLGDDPEFSDYNRTVMRWTGKWLEPTI 329	A; Molecule typ A; Residues: 1	pe: Dr -8563

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osyltrehalose trehalohydrolase - Mycobacterium tuberculosis (strain
terium tuberculosis
8 *sequence_revision 17-Jul-1998 *text_change 29-Sep-1999
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R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
ng the biology of Mycobacterium tuberculosis from the complete geno
: A70500; MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon es, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. 4, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : GB:Z74020; GB:AL123456; NID:g3261584; PIDN:CAA98329.1; PID:e24853 rce: strain H37Rv
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myces hygroscopicus
9 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
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A;Cross-references: EMBL:X86780; NID:9987088; PID:9987100; PIDN:CAA60460.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRARQQDAMESNFEFVESRRMIGLMRDDVAARALDVLVPLRHAAW-GANMNN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----- 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --ARQPDGVHARSQRWEPPGQFGAARTD------TGWPGRSVEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VADPVELFI-AQNLALDGLLYPLVYD------RFVD------ER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Mismatches 108; Indels 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.7%; Score 99; DB 2; Length 580; 19.8%; Pred. No. 0.99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVAARALQDAGRAALDEVREQFHARAARLG 328
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                                                                         || :|:
|SLFAKLPAGTTDKEEI 352
-----AGRAALDEV 316
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<COL>
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C;Genetics: A;Gene: rapA	856 ETATAQAQSAAQAARDRDGAWAALRAERAPLLDGQPTALHRSRE
Query Match 5.7%; Score 97.5; DB 2; Length 8563; Best Local Similarity 24.5%; Pred. No. 43; Matches 95; Conservative 34; Mismatches 154; Indels 105; Gaps 21;	CY 23* VDEALALDEGGARVAMILIAFMEENKMILDAVVRIMAMEEDINNKALLAKWIRDWAAKA 293   : :
IYRPIWDPDYEIFDPS              LDPE	:         :      :  921 QAALAAAEARAAETA-RAASEAATAQRAAEADLA
QY 64 SAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRR 107    1	RESULT 12 670932 probabe monoxygenase cytochrome P450 Rv0568 - Mycobacterium tuberculosis (strain H37 N;Contains: oxidoreductase (EC 1)
QY 108 MIGLMRDDVAARALDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHA 158  Db 585VHTGPSDLPVPEHAAAWDAIRREQTENPGVFVVIDVDFDDADPDPDDTLLRA 636	<pre>C;Species: Mycobacterium tuberculosis C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Mar-2000 C;Accession: G70932 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon</pre>
QY 159 MDNLGVAQYLTRLALAMAEPDVLEAAKATWIRDAAWQPLRRYVEDTLVV 207  10	; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998 A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
OY 208 ADPVELFIAQNLALDGLLYPLVYDRFVDERIALDEGGSAVAMLTAF 252	A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A. Reference number: A70500; MOID:98295987 A; Reference number: A70932 A; Accession: G70932 A; Status: preliminary; nucleic acid sequence not shown; translation not shown
OY 253 MPEWHTESNRWIDAVVKTWAAESDDNRALLARWTRDWSARAEAALAPVAARALQ 306  DD 745 GPEVHDLTPGDRVFGLVGSAFGGVAITDRRLLGAIPDTWSFTTAASIPIVFATAYYGLVD 804	A;Molecule type: DWA A;Molecule type: DWA A;Residues: 1-472 <col/> A;Residues: 1-472 <col/> A;Cross-references: GB:AL021942; GB:AL123456; NID:g3242298; PIDN:CAA17439.1; PID:e125 A;Experimental source: strain H37Rv
Qy 307DAGRAALDEVREQFHARAARLGIA 330  Db 805 LSGLSAGETVLIHATAGGVGMA 826	C;Genetics: A;Gene: Rv0568 C;Superfamily: Bacillus cytochrome P450 CYP106; cytochrome P450 homology C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase F;388/Binding site: heme iron (Cys) (axial ligand) *status predicted
RESULT 11 T03465 probable exonuclease (EC 3.1.15) - Rhodobacter capsulatus C; Species: Rhodobacter capsulatus	Query Match 5.3%; Score 91.5; DB 1; Length 472; Best Local Similarity 25.2%; Pred. No. 3.3; Matches 41; Conservative 20; Mismatches 69; Indels 33; Gaps 4;
C, Date: 24 mai 1959 *Sequence_revision 24 mai 1959 *text_change 1/ mar 2000 C; Accession: T03465 R; Vlock, C.; Paces, V.; Maltsev, N.; Paces, J.; Haselkorn, R.; Fonstein, M. Proc. Natl. Acad. Sci. U.S.A. 94, 9384-9388, 1997 A; Title: Sequence of a 189-kb segment of the chromosome of Rhodobacter capsulatus SB1003	162
A; Meterence number: %14935; MUID:9/404404 A; Accession: T03465 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA	QY 222 DGLLYPLVYDRFVDERIALEGGSAVAMLTAFMPEMHTESNRWIDAVVKIMAAESDDNRA- 280
A; Residues: 1-1238 <vlc> A; Cross-references: EMBL: AF010496; NID: 93128256; PIDN: AAC16118.1; PID: 93128266 C; Genetics: A; Genetics: SpcC</vlc>	QY 281LLARWTRDWSARAEAALAPVAARALQDAGRAALDEVREQ 319  L
A;Map position: 1 C;Superfamily: conserved hypothetical P115 protein C;Keywords: DNA repair; exonuclease; hydrolase	;
Query Match 5.6%; Score 96; DB 2; Length 1238; Best Local Similarity 26.0%; Pred. No. 4.7; Matches 72; Conservative 26; Mismatches 109; Indels 70; Gaps 10;	CiSpecies: Delinococcus radiodurans C;Species: Delinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000 C;Accession: C75525 R;White, 0:: Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
QY 64 SAIRMANWYALKDPRQEYYASWATTRARQODAMESNEEFVESRRMIGLMRDDVAARALDV 123	<pre>in, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, J.C.; Fraser, C.M. 999 of the radioresistant bacterium Deinococcus radiodurans F</pre>
OY 124 LVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQ-YLTRLALAMAEPD- 179  1	A; Kererence number: A/5250; MOID:20036896 A; Accession: C75525 A; Status: preliminary A; Molecule type: DNA
OY 180VLEAAKATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGLLYPLVYDRF 233	A;Residues: 1-697 <whi> A;Cross-references: GB:AE001899; GB:AE000513; NID:g6458070; PIDN:AAF09974.1; PID:g645 A;Experimental source: strain R1</whi>

C;Genetics: A;Gene: DR0397 A;Map position: 1	Db 137 RGEYRGRGLPDEVSLNRAVTEQRKGKTVTNKTSEQQFDALNKYGTDLTQRARDGKFDPVI 196 Qy 197LRRYVEDTLVVADPVELFIAQNLALDGLLYPLVYDRF 233
C;Superfamily: formate dehydrogenase	Db 197 GRDEEIRRVMQILLERSKNNPVLIGEPGVGKTAIAEGLAMRIVKGDVPEGLR 248
Query Match 5.3%; Score 90.5; DB 2; Length 697; Best Local Similarity 20.7%; Pred. No. 6.6; Matches 64; Conservative 32; Mismatches 106; Indels 107; Gaps 15;	OY 234 VDERI-ALEGGSAVAMLTAEMPEWHTESNRWIDAVVKTMAAESDDNRALLARWTRD 288
QY 60 DPSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRR 107	QY 289 WSARAEAALAPVAARA-LQDAGRAALDEVRE 318 
QY 108MIGLMRDDVAARALDVLVPLRHAAWGANMNNA 139 :   :	
OY 140 QICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAMAEPDVLE 182	
OY 183 AAKATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGLLYPLVYDRFVDRFYDERIALEG 242	Egland, P. Ibmitted to Description Reference
Qy 243 GSAVAMIJAFWPEWHIESNRWIDAVVKTMAAES-DDNRALLARWIRDWSARAEAALAPVA 301	A;Contents: correction A;Accession: A58538 A;Molecule type: DNA A;Residues: 1-539 < EGL>
	Cross-references Gibson, J.; Disp Bacteriol 176
Db 304 ADEVRDFAR 312	A.Title: 4-hydroxybenzoate-coenzyme A ligase from Rhodopseudomonas palustris: purific A.Reference number: A36960; MUID:94131941
RESULT 14 G75442 ATP-dependent Clp proteinase, ATP-binding subunit ClpB - Deinococcus radiodurans (strain	Artcession: A30900 Artstus: significant sequence differences Artstus: significant sequence differences Artstus: Associated (B:U02033; NID:9665919
C;Species: Deinococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000 C;Accession: G75442	C;Genetics: A;Gene: hbaA C;Gunerfamily: human SA nrotein: acetateCoA lidase homology
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; , M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Md S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.	Cymperimity: manda a process contract to the contract of the c
Science 260, 12/1-12/1, 1999 A)Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans RI. A)Reference number: A75250; MUID:20036896 A)Accession: G75442	Query Match 5.2%; Score 90; DB 2; Length 539; Best Local Similarity 20.8%; Pred. No. 5.2; Matches 65; Conservative 32; Mismatches 93; Indels 122; Gaps 16;
I> COOLDER, WATER SERENZAS, WITH SEARCH CONTRACTOR OF THE SEARCH CONTRA	107 RMIGLMRDDVAARALDVLVPERHAAWGANMNNAQICALGYGT
A.Experimental source: strain R1 C.Genetics: Continue of the strain R1 C.Genetics:	UD 190 KKIGIREDDVVFSAANLFFAIG-LENGMECFMGIGAISVLIFEKFIGUSVFDIL 230 Qy 149VFTAPAMFHAMDNLGVAQYLTRLALAMAEP 178
A;Gene: DRL046 A;Map position: 1 C;Superfamily: endopeptidase Clp ATP-binding chain	:    ::    251 RLHQPTLLFAVPTLYAAMLADPRSRTETL
/ Match 5.3%;	QY 179DVLEAAKATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGLLYPLVYDR 232   : :
<pre>best Local Similarity 23.5%; Pred. No. 8.9; Matches 78; Conservative 37; Mismatches 109; Indels 107; Gaps 17; Ov 76 DPROFYYASWATTRAROODAMES-NFEFVESRRMIGIMRDDVARALDVLVPLRHAAWGA 134</pre>	QY 233 -FVDERIALEGGSAVAMLTAFWPEWHTESNRWIDAVVKTMAAESDD 277
25	278 NRALLARWIRDWSARAEAALAPVAARALODAGRAAL
QY 135 NMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLAL 173 ::	Db 412 IFKVSGIWVSPFEIEQALMSHAKVLEAAVIPAEDTDGLIKPKAFIVLASRGDIDPG-ALF 470 Qy 314 DEVREQFHARAA 325
QY 174AMAEPDVLEAAKATWTRDAAWQP 196	Db 471 DELKEHVKSA 480

Search completed: September 26, 2000, 20:24:12 Job time: 3636 sec

luis Page Blank (uspto)

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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using sw model OM protein - protein search, September 26, 2000, 20:22:56 Run on:

; Search time 58.11 Seconds (without alignments) 176.517 Million cell updates/sec

US-09-430-029-3

1723 1 MTIELKTVDIKPLRHTFAHV.....ALDEVREQFHARAARLGIAL 331 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

85661 seqs, 30989116 residues Searched:

hits satisfying chosen parameters:

85661

Total number of

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Match 100% Post-processing: Minimum Match 0% Maximum

SwissProt\_38:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	. + 4	Description	P19730 pseudomonas	Q00460 pseudomonas	-		Q47096 erwinia car	P18798 methylococc	Q10769 mycobacteri	-			_			Q9z3q8 rhizobium m				Q50864 myxococcus	P22406 streptomyce	_	nicotiana	P15797 nicotiana t	P96489 streptococc	069733 mycobacteri	Q9ycy3 aeropyrum p	bacillus s	P50889 leuconostoc	P52477 pseudomonas	050323 synechococc			377	P27696 klebsiella
SUMMARIES	ţ	TT.	DMPL_PSESP	TMOE_PSEME	MEMB_METTR	GUNN_ERWCA	GUNV_ERWCA	MEMB_METCA	YF62_MYCTU	Y568_MYCTU	KLB2_ECOLI	GUNW_ERWCA	GATB_MYCLE	VLTF_BPT5	Y2G8_MYCLE	RHSE_RHIME	YJJK_ECOLI	UCR2_EUGGR	GATB_MYCTU	RFBC_MYXXA	REP_STRLI	E13B_NICPL	E13F_TOBAC	E13B_TOBAC	PROA_STRTR	Y2G8_MYCTU	SYM_AERPE	DHBF_BACSU	RS1_LEULA	MEXA_PSEAE	CH61_SYNVU	MFD_MYCTU	YD88_SYNY3	YODO_MYCTU	ILVB_KLEPN
	g	9	<del>, -</del> ;	1	Н	Н	Н	<b>—</b>	Н	-	Н	П	П	Н	-	٦	7	⊣	-1	1	-	_	Н	-	-	~	Н	Н	<del>, -</del> 1	H	Н	Н	H	Н	Н
	Query Match Length	renden.	331	326	394	444	202	386	580	472	461	204	209	1396	573	454	554	474	509	1275	456	365	370	371	416	573	572	1278	429	383	544	1234	154	431	559
al	Query		45.2	10.7	7.1	6.2	6.1	0.9	5.7	5,3		5.1	5.1	5.1	5.0	5.0	5.0	5.0	5.0	2.0	4.9	4.9	4.9	4.9	4.8						4.7		•	4.7	4.7
	Score	30016	779.5	184	123	106	105	103	66	91.5	88.5	88.5	88.5	87.5	87	86.5	86.5	85.5	85.5	85.5	85	84.5	84.5	84.5	83	83	82.5	82.5	82	81.5	81.5		81	81	81
	Result		7	2	m	4	'n	9	7	œ ·	ָא אַ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

P38217 saccharomyc P18014 shiqella fl		P27128 escherichia	F18009 Snigella II P96875 mycobacteri	P55127 neisseria m	053160 mycobacteri	P33349 escherichia	P55021 streptomyce
IMB2_YEAST IPA7_SHIFL	CH60_CYAPA CLPC_BACSU	RFAI_ECOLI	CIPC_MYCTU	FRPC_NEIME	CTPD_MYCTU	YEHM_ECOLI	SECA_STRLI
						Н	-
918	541 810	339	718	1829	657	759	947
4.7	4.6	4.6	4.6	9.4	4.6	4.6	4.6
80.5	80 80	79.5	79.5	79.5	79	79	79
34 35	36	80 C	40	41	43	44	45

## ALIGNMENTS

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                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
PHENOL HYDROXYLASE P1 PROTEIN (EC 1.14.13.7) (PHENOL 2-MONOOXYGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- COFACTOR: FAD, AND REQUIRES FE(+2) FOR ACTIVITY.
-:- PATHWAY: FIRST STEP OF PHENOL BIODEGRADATION.
-:- SUBUNIT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED BY P0, P1, P2, P3, P4 AND P5 POLYPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBMILTER (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATABOLIZES PHENOL, AND SOME OF ITS METHYLATED
DERIVATIVES: PI IS REQUIRED FOR GROWTH ON PHENOL, AND FOR
IN VITRO PHENOL HYDROXYLASE ACTIVITY.
-!- CATALYIC ACTIVITY: PHENOL + NADPH + O(2) = CATECHOL + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D28864; BAA06015.1; -.
PIR; B37831; B37831.
Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase; NADP; Flavoprotein; FAD; Iron; Plasmid.
SEQUENCE 331 AA; 38208 MW; 8042F5723BE3A5E8 CRC64;
                                                                                                                                                                                                                                                                                        MEDLINE; 91072230.
Nordlund I., Powlowski J., Shingler V.;
"Complete nucleotide sequence and polypeptide analysis of multicomponent phenol hydroxylase from Pseudomonas sp. strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.2%; Score 779.5; DB 1; Length 331; 46.8%; Pred. No. 5.3e-60; tive 54; Mismatches 115; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takeo M., Maeda Y., Okada H., Miyama K., Mori K., Ike M.,
                                         331 AA
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                   Bacteriol. 172:6826-6833(1990).
                                                                                                                                                                                           Pseudomonas sp. (strain CF600). Plasmid pVI150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M60276; AAA25940.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 46.8
Matches 155; Conservative
                                                                                                                                                                                                                                 Bacteria; Proteobacteria.
                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                      P1 COMPONENT)
DMPL OR PHEA2
                                 DMPL_PSESP
P19730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fujita M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BH;
KESULT 1
                                                                                                                                                                                                                                                                                                                                                                   CF600.
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4,

Gaps

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                                                                                                                                                                            LDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAM~-AEP 178
                                                                                                                                                                                                                                                                                                           ALEGGSAVAMLTAFWPEWHTESNRWIDAVVKTMAAESDDNRALLARWTRDWSARAEAALA 298
                                                                            PSRSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARA 120
MTIELKTVDIKPLRHTFAHVAQNIGGDKTATRYQEGMMGAQPQENFHYRPTWDPDYEIFD 60
                                                                                                                                                                                                                                                     : |: ||| | | | || ||||||||| |: EALDQAKAYWLDDPIWQGLRRYVEDSFVIRDWFEIGLAQNLVLDGLLQPLMYQRF-DQWL
                      MEDLINE; 91358306.

YEAR K.-M., Karl M.R., Blatt L.M., Simon M.J., Winter R.B.,
Fausset P.R., Lu H.S., Harcourt A.A., Chen K.K.;
"Cloning and characterization of a Pseudomonas mendocina KRI gene
                                                                                                                                                                                                                                 DVLEAAKATWTRDAAWQPLRRYVEDILVVADPVELFIAQNLALDGLLYPLVYDRFVDERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- COFACTOR: FAD; REQUIRES FE(+2) FOR ACTIVITY.
-!- PATHWAY: FIRST STEP IN TOLUBE DEGRADATION.
-!- SUBJULT: THE MULTICOMPONENT ENZYME TOLUBINE-4-MONOXYGENASE
-! SUBJULT: THE MULTICOMPONENT ENZYME TOLUBINE-4-MUNDOXYGENASE
IS FORMED BY THE TMOA, TMOB, TWOC, TWOD, TWOE AND TMOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aromatic hydrocarbons catabolism; Oxidoreductase; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
TOLUBENE-4-MONOOXYGENASE SYSTEM PROTEIN E (EC 1.14.13.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               084EE106D06FB5EC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cluster_encoding toluene-4-monooxygenase.";
J. Bacteriol. 173:5315-5327(1991).
-!- FUNCTION: HYDROXYLATES TOLUENE TO FORM P-CRESOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 AA
                                                                                                                                                                                                                                                                                                                                                                                                       |:| | | | |||||| | | ::|:
PLAEEA---TGIAALDEVRSAFATRLQKIGL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 1-14.
                                                                                                                                                                                                                                                                                                                                                                                     299 PVAARALQDAGRAALDEVREOFHARAARLGI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38255 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M65106; AAA26003.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monooxygenase; FAD; Iron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas mendocina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IS FORMED BY POLYPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TMOE PSEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=KR1
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Gaps

48;

Length 326;

10.7%; Score 184; DB 1; Length 326 22.4%; Pred. No. 9.9e-09; tive 60; Mismatches 134; Indels

Conservative

Query Match Best Local Similarity Matches 70; Conserv

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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: RESPONSIBLE FOR THE INITIAL OXYGENATION OF METHANE TO METHANOL IN METHANOTROPHS. IT ALSO CATALYZES THE MONOHYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-REB-1994 (Rel. 28, Last annotation update)
METHANE MONOOXYGENASE COMPONENT A BETA CHAIN (EC 1.14.13.25) (METHANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions on
ng as its content is in no
                                                                                                                         49 PMNLWYKQYRNASPLKHDNWDAFTDPDQLVYRTYNLMQDGQESYVQSLFDQFNEREHDQM 108
                                                                                                                                                                                                          109 VREGWEHTMARCYSPLRYLFHCLOMSSAYVOQMAPASTISNCCILQTADSL---RWLTHT 165
                                                                                                                                                                                                                                                                                          166 AYRTHELSLIYPDAGLGEHERELWEKEPGWQGLRELMEKQLIAFDWGEAFVSLNLVVKPM 225
                                       48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAD(P)(+) + H(2)O.
SUBJUIT: M.TRICHOSPORIUM HAS TWO FORMS OF METHANE MONOOXYGENASE, A SOLUBLE AND A MEMBRANE-BOUND TYPE. THE SOLUBLE TYPE CONSISTS OF THREE COMPONENTS (A, B AND C): PROTEIN A, COMPRISING THREE CHAINS, IN AN ALPHA-2, BETA-2, GAMMA-2 CONFIGURATION, IS A NONHEWE IROW PROTEIN CONTAINING AN UNUSUAL MG-HYDROXO BRIDGE STROCTURE AT ITS ACTIVE SITE AND INTERACTS WITH BOTH OXYGEN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 91251762.
Cardy D.L.N., Laidler V., Salmond G.P.C., Murrell J.C.;
"Molecular analysis of the methane monooxygenase (MMO) gene cluster
of Methylosinus trichosporium OB3b.";
Mol. Microbiol. 5:335-342(1991).
                                                                                                                                                                                                                                                                                                                                                           -MRKKPSEYDIVSRKLHY - STNNPDSPWELSPDS
                                                                                                                                                                112 MRDDVAARALDVLVPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRL
                                                                                                                                                                                                                                                 172 A----LAMAEPD--VLEAAKATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGL
                                                                                                                                                                                                                                                                                                                                 225 LYPLVYDRFYDERIALEGGSAVAMLTAFMPEWHTESNRWIDAVVKTMAAESDDNRALLAR
                                                                                --RSAIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF A VARIETY OF UNACTIVATED ALKENES, ALICYCLIC, AROMATIC AND HETEROCYCLIC COMPOUNDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Methylocystaceae; Methylosinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- CATALYTIC ACTIVITY: METHANE + NAD(P)H + O(2) = METHANOL +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Monooxygenase; NADP; One-carbon metabolism.
SEQUENCE 394 AA; 45020 MW; FA6C8F0970F28B90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. Thuse by non-profit institutions as long
KPLRHTFAHVAQNIGGDKTATRYQEGMMGAQPQE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MMOY.
Methylosinus trichosporium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                    285 WIRDWSARAEAA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 WIEKWRPLADRA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S15208; S15208.
                                    6 KPMR-TWSHLAE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYDROXYLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEMB_METTR
P27354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEMB METTR
                                                                                63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qq
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                                           14;
                                                                                                                                                                                                                                        129 HAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQ--YLTRLALAMAEPDV---LEA 183
                                                                                                                                                                                                                                                                                                                                                                                                   243 GSAVAMLTAFWPEWHTESNRWIDAV-VKTMAAESD---DNRALLARWTRDWSARAEAALA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                        277 DILIPFFTAQSQTYFQTTRGAIDDLFVYCLANDSEFGAHNRTFLNAWTEHYLASSVAALK 336
                                                                                                                                                            73 ALKDP-RQFY--YASWATTRARQQDAMESNFEFVESRRMIG-LMRDDVAARALDVLVPLR 128
                                                                                                                                                                                                   100 RHRDPARRWHHPYVKDKSEEARYTQRFLAAYSSEGSIRTIDPYWRDEILNKYFGALLYSE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olsen O., Thomsen K.K., Weber J., Duus J.O., Svendsen I., Wegener C., von Wettstein D.;
                                           Gaps
                                                                                                                     47 KPLSEYEQLSCYAQPNPDWIAGGLDWGDWTQKFHGGRPSWGNE----STELRTTDWY 99
                                                                                -- ENFH-YRPTWDPDYEIFDPSRSAIRMANWY 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LINKAGES IN CELLULOSE.
SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Transplanting two unique beta-glucanase catalytic activities into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŝ
                                                                                                                                                                                                                                                                                160 YGLFNAHSSVGRDC---LSDTIRQTAVFAALDKVDNAQMIQMERLFIAKLVPGFDASTDV
                                                                                                                                                                                                                                                                                                                       184 AKATWIRDAAWQPLRRYYEDTLV-VADPVELFIAQNLALDGLLYPLVYDRFVDERIALEG
                                                                                                                                                                                                                                                                                                                                                        217 PKKIWTTDPIYSGARATVQEIWQGVQDWNEILWAGHAVMIATFGQFARREFFQRLATVYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ENDOGLUCANASE N PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                one multienzyme, which forms glucose.";
Biotechnology 14:71-76(1996).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
                                           42;
Length 394;
Score 123; DB 1; Length 39
Pred. No. 0.0022;
9; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 1397.0., PPAM; PPO0942; CBD_3; 1. PFAM; PF00150; cellulase; 1. PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1. Cellulose degradation; Hydrolase; Glycosidase; 31 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       444 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENDOGLUCANASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               299 P-VAARALQDAGRAALDEVREQFHARAARLGI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 DFVGLYAKVEKSRA--DRSRRRLRGAAASSAI 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
                                         46;
7.1%; 22.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=ATROSEPTICA FCBR C18;
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                              28 KTATRYQEGMMGAQPQ-
                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Erwinia carotovora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CELLULASE N)
                                     74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUNN ERWCA
    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Erwinia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GUNN_ERWCA
                                           Matches
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                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOI. Gen. Genet. 241:341-350(1993).
-!- FUNCTION: ENDOGLUCANASE WITH SOME EXOGLUCANASE ACTIVITY. THE PH
OPTIMUM IS ABOUT 7.0 AND THE TEMPERATURE OPTIMUM ABOUT 42 DEGREES
                                                                                                                                                                                                                                                                                                                                                                                              112 MRDDVAARALDVLVPLRHAAWGANMNNAQI--CALGYGTVFTAPAMFH-----AMDNL 162
                                                                                                                                                                                                                                 ----W----QP 196
                                                                                                                                                                                                                                                                                                      237
                                                                                                                                                                                                                                                                                                                                                                          --ESNRWIDAVVKTMAAESDDNRAL-L 282
                                                                                                                                                                                            ------WGINVFRVAMYTAADGY ---ISNPSLANKVKEAVAAAQSL 121
                                                                                                                                                                                                                                                                  GVYIIIDWHILSDNDPNIYKAQAKTFFRAEMAGLYGSSPNVIYEIANEPNGGVTWNGQIRP 181
                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKAGES IN CELLULOSE.
SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL-
HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
LINOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ENDOGLUCANASE V PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE V)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 94067016.

Cooper V. U.C., Sallmond G.P.C.;
"Molecular analysis of the major cellulase (Celv) of Erwinia
"Molecular analysis of the major cellulase are carotovora: evidence for an evolutionary 'mix-and-match' of enzyme
                                                                                                                                                                                                                                                                                                                              YALEVTDTIRSKDPDNLIIVGTGTWSQDIHDAADNQLPDPNTLYALHFYAGTHGQFLRDR
                                                                                                                                                                                                                                                                                                      ---AQNLALD-GLLYPL----VYDRFVDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
                                                                                      6.2%; Score 106; DB 1; Length 444;
23.5%; Pred. No. 0.076;
Live 35; Mismatches 75; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                              283 ARWTRDWSARAEAALAPVAARA-----LODAGRAALDEVREOFHARAARLG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
FA7E4179004CBB43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     505 AA
                                                                                                                                                                                                                                 163 GVAQYLTRLALAMAEPDVLEAAKATWTRDAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                    48300 MW;
                                                                                                                                                                                                                                                                                                      197 LRRYVEDTLVVADPVELFI----
                                                                                                                                                                                                                                                                                                                                                                          I - - ALEGGSAVAMLTAFMPEWHT -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00942; CBD_3; 1.
PFAM; PF00150; cellulase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X76000; CAA53592.1; -.
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q06851; 1NBC
                                  444 AA;
                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erwinia carotovora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
168
256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-SCRI193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CELLULASE V).
                                                                                                                                                                                              81 LRDD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GUNV_ERWCA
Q47096;
                                                                                                                            :69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domains.";
 ACT_SITE
ACT_SITE
SEQUENCE
                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Erwinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GUNV_ERWCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                          Best_Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                           242
                                                                                                                                                                                                                                                                    122
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17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUNCTION: RESPONSIBLE FOR THE INITIAL OXYGENATION OF METHANE TO METHANOL IN METHANOTROPHS. IT ALSO CATALYZES THE MONOHYDROXYLATION OF A VARIETY OF UNACTIVATED ALKENES, ALICYCLIC, AROMATIC AND HETEROCYCLIC COMPOUNDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
METHANE MONOOXYGENASE COMPONENT A BETA CHAIN (EC 1.14.13.25) (METHANE
                                                                                                                                                                                                                                            112 MRDDVAARALDVLVPLRHAAWGANMNNAQI--CALGYGTVFTAPAMFH-----AMDNL 162
                                                                                                                                                                                                                                                                                                            --W----0P 196
                                                                                                                                                                                                                                                                                                                                      GVYIIIDWHILSDNDPNIYKAQAKTFFAEMAGLYGSSPNVIYEIANEPNGGVTWNGQIRP 181
                                                                                                                                                                                                                                                                                                                                                                    197 LRRYVEDTLVVADPVELFI-----AQNL--ALDGLL------YPLVYDRFVDER 237
                                                                                                                                                                                                                                                                                                                                                                                                   182 YALEVIDIIRSKDPDNLIIVGIGTWSQDIHDAADNQLPDPNTMYALHFYAGTHGOFLRDR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                238 I--ALEGGSAVAMLTAFMPEWHT-------ESNRWIDAVVKTMAAESDDNRAL-L 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDYAQSRGAAI-----FVSEWGTSDASGNGGPFLPESQTWIDFL-----NNRGVSW 287
                                                                                                                                                                                                                                                                         73; Indels 114; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         · ; :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAD(P)(+) + H(2)O.
SUBUNIT: M.CAPSULATUS HAS TWO FORMS OF METHANE MONOOXYGENASE,
A SOLUBLE AND A MEMBRANE-BOUND IYPE. THE SOLUBLE TYPE CONSISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosenzweig A.C., Frederick C.A., Lippard S.J., Nordlund P., "Crystal structure of a bacterial non-haem iron hydroxylase that catalyses the biological oxidation of methane.";
Nature 366:537-543(1993).
                                                                                         CELLULOSE-BINDING (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stainthorpe A.C., Murrell J.C., Salmond G.D.C., Dalton H., Lees "Molecular analysis of methane monooxygenase from Methylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 ARWIRDWSARAEAALAPVAARA-----LQDAGRAALDEVREQFHARAARLG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteobacteria; gamma subdivision; Methylococcacea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: METHANE + NAD(P)H + O(2) = METHANOL +
                                                                                                                                                                                    DB 1; Length 505;
              Cellulose degradation; Hydrolase; Glycosidase; Signal.
SIGNAL
                                                                                                                                        DBEA9337BB4D2623 CRC64;
                                                                                                                                                                         Score 105; Db 1
                                           ENDOGLUCANASE V.
                                                                                                                                                                                                   Pred. No. 0.11;
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        386 AA.
                                                                                                                                                                                                                                                                                                         163 GVAQYLTRLALAMAEPDVLEAAKATWTRDAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 1-40.
 GLYCOSYL_HYDROL_F5; 1.
                                                            CATALYTIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arch. Microbiol. 152:154-159(1989).
                                                                                                                                        MM;
                                                                                                                                                                                   6.18;
                                                                                                                                        54900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methylococcus capsulatus.
                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                           505
334
352
505
168
256
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01-NOV-1990 (Rel. 16,
01-OCT-1996 (Rel. 34,
                                           32
32
335
353
168
256
805 AA;
                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 89373399.
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 PROSITE: PS00659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   capsulatus (Bath),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Methylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYDROXYLASE)
                                                                                                                                                                                                                 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-BATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEMB METCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria;
                                                                                                                        ACT_SITE
SEQUENCE
                                                                                                        ACT_SITE
                                                                                                                                                                                   Query Match
Best Local
                                                                         DOMAIN
                                                            DOMAIN
                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEMB_METCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              242
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 KHRDPLRRWHAPYVKDKAE------EWRYTDRFLQGYSADGQIRAMN---PTWRTSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----WGANMNNAQICALGYGTVFTAPAM-------FHAMDNLGVAQ--YLTR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 CNRYWGAFLFNE----YG-LFNAHSQGAREALSDVTRVSLAFWGFDKIDIAQMIQLER 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SDYNRTVMRNWTGKW-----LEPII 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 ALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARALDVLVPLRHAA- 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 LALAMAEPDVLEAA---KATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGL--- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
OF THREE COMPONENTS (A, B AND C): PROTEIN A, COMPRISING THREE CHAIRS, IN AN ALPHA-2, BAWMA-2 COMPIGHRATION, IS A NONHEME IRON PROTEIN CONFIGURING AN UNUSUAL MU-HYDROXO BRIDGE STRUCTURE AT ITS ACTIVE SITE AND INTERACTS WITH BOTH OXYGEN AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 KTATRYQEGMMGAQPQ------ENFH-YRPTWDPDYEIFDPSRSAIRMANWY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 KRLTEYEALITVYAQPNADWIAGGLDWGDWTQKFHGGRPSWGNE-----TTELRIVDWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEWHTESNRWIDAVVKTMAAESDDNRALLARWTRDWSARAEAALAPVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---EVYKSARLAVEGLWQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93; Indels 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 98295987.

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., He Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 103; DB 1; Length 386; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Monooxygenase; NADP; One-carbon metabolism.
INIT MET 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----LYPLVYDRFVD----ERIALEGGSAVAMLTAFM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DF1DBB7BD16F0978 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 64.1 KDA PROTEIN RV1562C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GFLAKIVPGFDESTAVPKAEWTNG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 AA; 44590 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M90050; AAB62393.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RV1562C OR MTCY48.03. Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JL0101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                        METHANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JL0101;
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Q10769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INIT_MET
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YF62_MYCTU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254
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   SOUTH A WANTER COURT OF THE SOUTH 
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Sqares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 FYYASWATTRARQODAMESNFEFVESRRMIGLMRDDVAARALDVLVPLRHAAW-GANMNN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 AQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAMAEPDVLEAAKATWTRDAAWQPLR 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LMPVNSFAGTRGWGYDGVLWYSVHEPYGGPDGLVRFLDACHARRLGVLIDA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---ALKDPRQ 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEFRUWAPKPALVRLDVNGAVHAMTRSADGWWHITVAAPADARYGYLLDDDPTVLPDPRS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 IALEGGSAVAMLTAFMPEWHTESNRWIDAVVKTMAAESDDNRALL----ARWTRDWSA--
                                                                                                                                                 SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
SIMILARITY: TO M.TUBERCULOSIS RV1563C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 580;
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                                                                                                                                                                                                                                                                                                                                                                                                                              .l protein; Hydrolase; Glycosidase.
580 AA; 64076 MW; 506190468F44B862 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 -RAEAALAPVAARALQDAGRAALDEVREQFHARAARLG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 LRLDAVHALVDTTAVH-----VLEELANATRWLSGQLG 276
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PUTATIVE CYTOCHROME P450 RV0568 (EC 1.14.-.).
RV0568 OR MTV039.06.
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                                                                                         IUBERCULIST; RV1562C; -
PFAM; PF00128; alpha-amylase; 1.
Hypothetical protein; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
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(Rel. 39, Last seq
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                                                                                                                                 Nature 393:537-544(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 PDYEIFDPSRSAIRM ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Matches 6
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Y568_MYCTU
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                                                                                              J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 LGVAQYLTRLALAMAEPDVLEAAKATWTRDAAWQPLRRXVEDTLVVADPVELFIAQNLAL 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-237 FROM N.A.
Larsen M.H., Figurski D.H.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- DOMAIN: CONTAINS A DMA-BINDING REGION JOINED BY A SHORT VARIABLE SEGMENT TO A REGION SIMILAR TO E.COLI KORA AND TRBA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Baabadook K., Baabham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Shornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Osborns J., Osborns J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares T., Sulston J. Taylor K., Whitehead S., Barrell B.G.;

Taylor K., Whitehead S., Barrell B.G.;

Complete genome sequence.";

Nature 393:537-544(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pansegrau W., Lanka E., Barth P.T., Figurski D.H., Guiney D.G., Haas D., Hellinski D.R., Schwab H., Stanisloh V.A., Thomas C.M.; "Complete nucleotide sequence of Birmingham IncP alpha plasmids Compilation and comparative analysis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 472;
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                                                                                                                                                                                        SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          388 HEME (BY SIMILARITY).
50687 MW; B7E2898BEE80863F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Oxidoreductase; Monooxygenase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 GLSWALERLIRHPVILAKAVQAADASAAGDPAGDEYLDAVAKE 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69;
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Last sequence update)
Last annotation update)
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25.2%; Pred. No. 1.5;
tive 20; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               TUBERCULIST; RV0568; -.
PFAM; PF00067; p450; 2.
PROSITE; PS00086; CYTOCHROME_P450; 1.
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                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL021942; CAA17439.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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(Rel. 35, I
(Rel. 35, I
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Best Local Similarity
Matches 41; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 94285211.
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01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                            194 WQPLRRYVEDTLVVADPVELFIAQNLALDGLLYPLVYDRFVDERIALEGGSAVAMLT--- 250
                                                                                                                                                                                                                                                                                                                                                                                                                    142 -CALGYGTVFTAPAMFHAMD-----NLGVAQYITRLALAMAEPDVLEAAKATWTRDAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ARD-----QDRLADEPLP----AWLAGITPPP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 ARQQDAMESNFEFVESRRMIGLMRDDVAARALDVLVPLRHAAWG-----ANMNNAQI-- 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVESGYGGLITVHFQFHAVDLDGPFISETGYRSHYDHARGGMIVDQVADGVLRALLRSH- 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----AFMPEWHIESN-----RWIDAVVKIMAAESDDNRALLARWIRDWSARAEAALAPVA 301
                                                                                                                                                                                                                                                                                                                        Gaps
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ENDOGLUCANASE VI PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE VI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Structure and regulation of the Errinia carotovora subspecies carotovora SCC3193 cellulase gene celV1 and the role of cellulase in phytopathogenicity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL HYDROLASES).
                                                                                                                                                     EMBL; L2/100, '... AAS7449.1; -.
EMBL; U05773; AAS7449.1; -.
Plasmid; DNA-binding; Transcription regulation.
344 TO THE C-TERMINAL OF E.COLI KORA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                        . 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Gen. Genet. 247:17-26(1995).
- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC LINKAGES IN CELLULOSE.
                                                                                                                                                                                                                                                                                       1; Length 461;
                                                                                                                                                                                                                                                                                                                      73; Indels
                                                                                                                                                                                                                                   10EBFB2F2E00BD81 CRC64;
                                 ween the Swiss Institute of Bioinformatics
European Bioinformatics Institute. There a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           504 AA.
                                                                                                                                                                                                                                                                                    ; Score 88.5; Di
; Pred. No. 2.6;
31; Mismatches
                                                                                                                                                   EMBL; L27758; -; NOT_ANNOTATED_CDS.
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                                                                                                                                                                                                                                   51165 MW;
                                                                                                                                                                                                                                                                                     5.1%; 22.5%;
                                                                                                                                                                                                                                                                                                                   56; Conservative
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                   461 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 ARALQDAGR 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Erwinia carotovora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----RRYLD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    350 AKAQEPAGQ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SCC3193;
MEDLINE; 95231512.
                                                                                                                                                                                                                                                                                                                                                                                     171 AGDQDAAE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELLULASE V1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUNW_ERWCA
                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                     Local
               This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GUNW_ERWCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
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16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Oliver K., Harris D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (SEP-1997) to the EMBL/GenBank/DDDJ databases.

-! FUNCTION: FURNISHES A MEANS FOR FORMATION OF CORRECTLY CHARGED
GLN-TRNA(GLN) THROUGH THE TRANSAMIDATION OF MISACYLATED GLU-
TRNA(GLN) IN ORGANISMS WHICH LACK GLUTAMINIT.TRNA SYNTHETASE. THE
REACTION TAKES PLACE IN THE PRESENCE OF GLUTAMINE AND ATP THROUGH
AN ACTIVATED GAMMA-PHOSPHO-GLU-TRNA(GLN) (BY SIMILARITY).

-! CATALYTIC ACTIVITY: ATP + L-GLUTAMYL-TRNA(GLN) + L-GLUTAMINE = ADP
+ PHOSPHATE + L-GLUTAMINNI-TRNA(GLN) + L-GLUTAMINE = ADP
-! SUBUNIT: HETEROTRIMES FOR A, B AND C SUBUNITS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                112 MRDDVAARALDVLVPLRHAAWGAN-----MNNAQICALGYGTVFTAPAMFHAMDNLGVA 165
                                                                                                                                                                                                                                                                                                                                                                                                                              81 LRDDWGINVFRVAMYTAENGYIANPSLANKVKEAVAAAQGLGVYIIID--WHTLSDNDPN 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EC 6.3.5.-) (GLU-ADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 -FVSEWGTSDASGNGGPFLPESQTWIDFL-----NNRGISWVNWSLSDKSETSAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ESNRWIDAVVKTMAAESDDNRAL-LARWTRDWSARAEAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 QYLTRLALAMAE-----PDVL-EAA----KATWTRDAAWQPLRRYVEDTLVVADPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AQNLALD-GLLYPL----VYDRFVDERI--ALEGGSAVAMLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197 NLIIVGSGTWSQDIHDAADNQLPDPNTLYALHFYAGTHGOFLRDRIDYAQSRGAAI----
                                                                                                                                                                                                                                      CELLULOSE-BINDING (BY SIMILARITY). PROTON DONOR (BY SIMILARITY). NUCLEOPHILE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                  83;
                                                                                                                                                                                                                                                                                                                                   Length 504;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                           Glycosidase; Signal.
                                                                                                                                                                                                                                                                                      0D7ECF74781565FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                  :66
                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 VAGASKSGWTEQNLSTSGKF----VREQIRAGAGLSG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 APVAARA-----LQDAGRAALDEVREQFHARAARLG 328
                                                                                                                                                                                          ENDOGLUCANASE V1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
GLUTAMXL-TRNA(GLN) AMIDOTRANSFERASE SUBUNIT B
                                                                                                                                                                                                                                                                                                                                 Score 88.5; DB Pred. No. 2.9; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  509
                                                                                              HSSP; QU6851; 1005.7 1.

PFAM; PF00942; Cellulase; 1.

PROSITE; PS00659; GLXCOSYL_HYDROL_F5; 1.

Cellulose degradation; Hydrolase; Glycos
                                                                                                                                                                                                          CATALYTIC.
                                                                                                                                                                                                                           LINKER
                                                                                                                                                                                                                                                                                                                                                                  31;
                                                                                                                                                                                                                                                                                     54963 MW;
                                                                             EMBL; X79241; CAA55823.1; -.
                                                                                                                                                                                                                                                                                                                                                     23.48;
                                                                                                                                                                                                                                                                                                                                                Similarity 23.49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                       334
352
504
168
256
                                                                                                                                                                                                                                     353
168
256
504 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLCB637.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 ELFI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251 AFMPEWHT---
                                                                                                                                                                                          32
32
335
                                                                                                                                                                                                                                                                                                                                                                  65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT B)
                                                                                                                                                                                                                                                    ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                     Sest Local
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                                                                                                                                                                         SIGNAL
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DOMAIN
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                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                              330 LP-----WLSRKRIQQEWGISD-----EVMRDLVNAGAVELVAATVKNGASSE 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RHAAWGANM-----NNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAMAEPDVLE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TLDELAITPAQVAVVALVDEGKLS 416
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 ILVSGGRIAQETRHFHEDGYTSPGRAKETAQDYRYFPDPDLEPVAPSRELVEQLRQTIPE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               417 IRLA-------RQVVEGVLAGEGEPEQVMVDRDLAL--VRDDSVMQAAVDEALAAD 463
                                                                                                                                                                                                                                                                                                                                                       -- QNIGGDKT---ATRYQEGMMG- 39
                                                                                                                                                                                                                                                                                                                                                                                                                                 ---YRPTWDPDYEIFDPSRSAIRMANWYALK 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183 AAKATWIRDAAWQPLRRYVEDTLV-VADPVELFIAQNLALDGLLYPLVYDRFVDERIA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriophage T5.
Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
                                                                                                                                                                                                                                                                                                   Pred. No. 2.9;
; Mismatches 104; Indels 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kaliman A.V., Kryukov V.M., Bayev A.A.; "The nucleotide sequence of bacteriophage T5 DNA at the region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleotide sequence of the bacteriophage T5 ltf gene."; Lett. 366:46-48(1995).
                                                                                                                                                                                                                                                                                 DB 1; Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaliman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.
Kryukov V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 DPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARALDVLVPL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 -----LEGGSAVAMLTAFMPEWHIESNRWIDAVVKTMAAESDDNR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----AGAIVGAVMKTTRGQADAAR 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                           A6E2730FF92C264D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1996 (Rel. 33, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
L-SHAPED TAIL FIBER PROTEIN (LTF PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1396 AA
                                                                                                                                                                                                                                                                             5.1%; Score 88.5;
19.9%; Pred. No. 2.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between early and late genes.";
Nucleic Acids Res. 16:6230-6230(1988).
                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                 PFAM; PF01162; PET112; 1.
PROSITE; PS01234; PET112; 1.
Protein blosynthesis; Ligase.
SEQUENCE 509 AA; 55361 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P13390; 048502;
01-JAN1990 (Rel. 13, Created)
01-FEB-1996 (Rel. 33, Last sequ
15-FEB-2000 (Rel. 39, Last and
                                                                                                                                                                                                                                                                                                                                                       5 LKTVDIKPLR-----HTFAHVA-
                                                                                                                                                                                                                                                                                                                                                                                                                               -----AQPQENFH------
                                                                                                                                                 EMBL; Z99263; CAB16430.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 QARAWGNFLVQKANEANI --
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464 PDVAEKIRGGKVAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 95309401.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VLTF BPT5
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                                                                                                                                                                                                                                                                                                                                                                                                                    16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1162 TRY-----IGATOPGSTF-YIGASGHDGEKFDSMRGSV-----AIKSA-----GGWGPTS 1205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1206 IPTQVVLET----CESGSISRLPRWGVDHNG--TLMPMADNRYNLGWGSG-RVKQVYAVN 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 ARQQDAMESNFEFVESRRMIGLMRDDVAARALDVLVPLR----HAAWGANMNNAQICALG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 YGTVFTAPAMFHAMDNLGVAQYLTRLALAMAEPDVLEAAKA------TWTRDAAWQPL 197
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 TRYQEGMMGA-QPQENFHYRPTWDPDYEIFDPSRSAIRMANWYALKDPRQFYYASWATTR 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
  NONESSENTIAL PROTEIN THAT MEDIATES BINDING TO THE
                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SIGNIEGER K., Garnier T., De Rossi E., Fsihi H., Cole S.T.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CBXX/CFQX FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1305 REHC--GLIVQRAIE--IMESFGLDPFKYGFICYDKWDEHIVVSEYGPA 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 RRYVEDILVVADPVELFIAQNLALDGLLYPLV-YDRFVDERIALEGGSA 245
                                                                                                                                                                                                                                                                                                -> A (IN REF. 2).
18CD2192F65FFFC1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00819; CBXCFQXSUPER.
HYPOCHETICAL protein; ATP-binding.
MP_BIND 334 341 A341 SEQUENCE 573 AA; 62342 MW; A60CD0F7D73DD098 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-FEB-2000 (Rel. 39, Created)
15-FEB-2000 (Rel. 39, Last sequence update)
1F-FEB-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 62.3 KDA PROTEIN MLCB628.18C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             573 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               13;
                                                                                                                                                                                                                                                                                                                                                                           5.1%; Score 87.5; 26.2%; Pred. No. 13
                                                                                                                                                                                                                                                                                                                   147989 MW;
                                                                                                                                                                                                               EMBL; X69460; CAA49220.1; -. EMBL; AJ001191; CAA04591.1; PIR; S01982; S01982.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y14967; CAA75205.1; -.
                    POLYMANNOSE O ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00004; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                1396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                              986
                                                                                                                                                                                                                                                                             Late protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y2G8_MYCLE
033089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLCB628.18C.
                                                                                                                                                                                                                                                                                                                                                                                                                    90;
                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rhizobactin regulon.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: FAD (BY SIMILARITY).
-!- PATHWAY: RHIZOBACTIN SIDEROPHORE BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE LYSINE N6-HYDROXLYASE / L-ORNITHINE N5-OXYGENASE FAMILY.
                                                                                                  220 GNEDAAVALLEWLQTTHPESKVSAALKDPSYRLTTTTAEQIAARADPWDPSSVVTDNSDR 279
                                                                                                                                    65 AIRMANWYALKDPRQFYYASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARALDVL 124
                                                                                                                                                                    280 DRLLTQAQAELD-RQI-----GLTRVKTQ-----IERYRAATMMAKVRAAKGMKVA 324
                                                                                                                                                                                                    125 VPLRHAAWGANMNNAQICALGYGTVFTAPAMFHAMDNLGVAQYLTRLALAMAEPDVLEAA 184
                                                                                                                                                                                                                                                                                                    -----SAVKAAKTIDLALGGVLFIDEAYALVQER--DGRTD 411
                                                                                                                                                                                                                                                                                                                                        240 LEGGSAVAMLTAFMPEWHTESNRWIDAVVKTMAAESDD-----NRALLARW-TR---- 287
                                                                                                                                                                                                                                                                                                                                                                                 464
                                                                                                                                                                                                                                                                                                                                                                                                               --DWSARAEA-----ALAPVAARALQDAGRAALDEVREQFHAR 323
                                                                                                                                                                                                                                                                                                                                                                                                                                     465 TYSPDELLEIAKVIATDADSSLSAEASKNLLEAAKQLAQRACRTR--GRPALDVAGNGRYAR 522
                                                                                                                                                                                                                                           -----ISEPKLVETS 366
                                                                       --WDPDYEIFDPSRS 64
                                                                                                                                                                                                                                                                                                                                                               KATWTRDAAWQPLRRYVEDTLVVADPVELFIAQNLALDGLL----YPLVYDRFVDERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Iron transport; NADP; Flavoprotein; FAD; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (EC 1.-.-).
                                     Indels 118;
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Lynch D., O'Connell M., O'Brien J.;
"Cloning and sequence analysis of the Rhizobium meliloti 2011
     Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium meliloti (Sinorhizobium meliloti).
Plasmid pSymA (megaplasmid 1).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
Rhizobiaceae; Sinorhizobium.
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57074278FF4FC1D1 CRC64;
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15-FEB-2000 (Rel. 39, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
RHIZOBACTIN SIDEROPHORE BIOSYNTHESIS PROTEIN RHSE
5.0%; Score 87; DB 1; Let 22.8%; Pred. No. 4.5; ive 37; Mismatches 123;
                                                                                                                                                                                                                                      325 OPSKHMIFTG-----PPGTGKTTIARVVANILAGLGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA.
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                                                                   GGDKTATRYQEGMMGAQPQENF----HYRPT--
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                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                Similarity
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                                                                                                                                                                                                                                                                                                        RKDFVAEYEGO-
                                 82;
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Q9Z3Q8;
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Best Local S
Matches 66
Query Match
Best Local
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16;

Gaps

79;

Indels

102;

DB 1; Length 454;

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79 QFY--YASWATTRARQQDAMESNFEFVESRRMIGLMRDDVAARAL--DVLVPLRHAAWGA 134
                                                                                                                                                                                                                                                                           135 NMNNAQICALGYGT-----VFTAPAMFHAMD-------NLGVAQYLTR 170
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the
                                                                                                                                                                                                                                                                                                                       202 CVLALLNDLIPEMVAAGASIQWITRSAGFFPMEYSKLGLEYFTPDYMRHFHRIAPVRRRE 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-KI2 / MG1655,
MEDLINE: 97426617.
Blatther F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Rliety M., Collado-Vides J., Glasner F.D., Rode C.K., Maybew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                         36 KPAFRWHEGLILPGTTLQVPFMADLVTMADPTHRLSFLNYLAVHDRLYKFYFYENFMIPR
28 KTATRYQEGMM--GAQPQENF--HYRPTWDPDYEIFDPSRSAI--RMANWYALKD---PR
                                                                                                                                                                                                       96 QEYDHYCRWA---SQQLSACRFGEEVV------DVAHESASDSFIVESRSASGGK
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Bright H., Razemier B., Keck W.;

Murein-metabolizing enzymes from Escherichia coli: sequence and controlled overexpression of the slt gene, which encodes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blattner F.R., "Analysis of the Escherichia coli genome VI: DNA sequence of region from 92.8 through 100 minutes.", Nucleic Acids Res. 23:2105-2119(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 99420866.
Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs I
"Enrichment of low abundance proteins of Escherichia coli by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 95334362.
Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       206 VVADPVELFIAQNLALDGLLYPLVYDRFV---DERIALEGGSAVAML 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 IVADQGLLYKGISFSTIGEIFDLMYERSVGGRDPGLALFSNCAVETL 308
                                                                                                                                                                                                                                                                                                                                                                                                                 171 LALAMAE---PDVLEA-AKATW-TRDAAWQP-----LRRYVEDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Last Sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
ABC TRANSPORTER ATP-BINDING PROTEIN YJJK.
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IDENTIFICATION BY MASS SPECTROMETRY.
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J. Bacteriol. 173:6773-6782(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 30, Created)
(Rel. 36, Last seq
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REVISIONS TO C-TERMINUS.
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MEDLINE; 97443975.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 DAMESNFEFVESRRMIGLMRDDVAARALDVLVPLRHAAWGANMNNAQICALGYGTVFTAP 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | | | :::
14 VPPKRHILKNISLSFFFPGAKIGVLGLNGAGKSFLLRIMAGIDKDIEGEARPQPDIKIGYL 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 PQENFHYRPIWDPDYEIFDPSRSAI------RMANWYALKDPRQFYYASWAITRARQQ 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----MGAQ 41
hydroxyapatite chromatography.";
Electrophoresis 20:2181-2195(1999).
-!- SIMILARITY: BELONGS TO THE APP-BINDING TRANSPORT PROTEIN FAMILY
(ABC_IRANSPORTERS). EF-3 SUBFAMILY. STRONG, TO H.INFLUENZAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 AVVKTMAAESDDNRALLARWIRDWSARAEAALAPVAARALQDAGRAAL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 129;
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: 444C605C67A019B1 CRC64;
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EMBL, M69185; -; NOTANNOTATED_CDS.
ECOGENE; EG12343; VJJK.
PFAM; PF00005; ABC_tran; 2.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
APP-binding; Transport; Repeat.
INIT_MET
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45
362
62311 MW; A
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355 3
554 AA;
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   RRI RELEASE DE LA DESTRETA DE LA DES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \delta V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΩD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QΥ
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Search completed: September 26, 2000, 20:30:02 Job time: 426 sec

luis bade Blank (nsbto)

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

September 26, 2000, 20:11:41; Search time 75.19 Seconds (without alignments) 28.036 Million cell updates/sec Run on:

US-09-430-029-4

451 1 MSNVFIAFQANEDSRPIVDA.....ITLSGHIDEDDDEFTLSWSH 89 Title: Perfect score: Sequence:

Scoring table:

188963 seqs, 23686106 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Toluene ortho-mono	Alcaligenes sp. pr	Protein containing	β	Sequence of a regi	ali	Wheat S-adenosylme	Amino acid sequenc	Sequence of the S1	S-adenosylmethioni	S-adenosylmethioni	S-adenosylmethioni	Cytochrome enzyme	Yeast presequence	Seguence of beta-c	Serine protease Pf	Human apoAIV mutei	Human apoAIV mutei	A serine/threonine	Spike protein of i	vine leafrol	AFT-1 interacting	•			- 1		CD2 associated int	ated	Acylamino acid-iso	Protein encoded by	Ξ	GLVR-1 protein. Ne
SUMMAKLES		QI	W06801	W98972	R51368	R40815	P70137	W06829	W97744	W80988	72	W34540	W34541	W34542	R11349	R61118	R20982	W01203	R39490	R39491	W67642	R11611	W73476	R89748	W25116	W26496	W80420	W25115	W26495	W80419	W37724	R11056	27	147	R72970
		Length DB	92 1																															117 1	
æ		Match Len	.7	0.	0.	4.	. 4	4.	٤.	7.	7.	٦.	г.	۲.	6.	٠.	٠.	٠.	₽.		Φ.		7.	7.	3.2	3.2	3.2	3.2	3.2	7.	7	0.	σ.	12.9	6.
		Score	355	257	67.5	65	65	65	64.5	<b>64</b>	<b>64</b>	63.5	63.5	63.5	62.5	62	62	61	60.5	60.5	60.5	60.5	60.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	59.5	58.5	58	58	58
	Result		П	7	m	4	Ŋ	9	7	88	on	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59	30	31	32	33

The gibbon ape leu S. cerevisiae scau	Saccharomyces cere Fumonosin-resistan	Bovine P58 protein	A serine/threonine	Renal cancer assoc	Polyamide hydrolas	Polyamide hydrolas	DnaK protein. DnaK	H. pylori ORF 12ae	Streptomyces venez
W96999 R67691	W10424 Y06819	W36140	W67641	X07078	M29999	W36011	R94587	X11069	W19630
		Н	-	Н	Н	7	П	1	-
681	1477	504	1051	297	355	355	618	459	559
12.9	12.9	12.7	12.6	12.5	12.5	12.5	12.5	12.4	12.4
58 58	58 58	57.5	22	56.5	56.5	56.5	56.5	99	95
34 35	36 37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

AC I	
BB	
K K	<pre>tom: pTOM; self-transmissable; constitutive; bioreactor; pollutant; breakdown; trichloroethylene; TCE; degradation.</pre>
OS	Pseudomonas cepacia strain PR1-23.
PD	05-04-01/ A. 06-AUG-1996.
ΡF	02-MAY-1991; 694718.
PR DD	02-MAY-1991; US-694718. 15-DBC-1903: US-167/57
PR	15 DEC 1999, US 10/40/.
ΡA	(FRAN/) FRANCESCONI S C.
PA F	(SHEZ) SHIELDS M S.
7 Z	WPT: 96-370640/37
DR	N-PSDB; T44457.
ΡŢ	Microorganisms transformed with P. cepacia PR1-23 Tom enzyme gene
PT c	are useful for degradation of chloro; aliphatic cpds, and aromatics
ი შე	Ciarm 1; COLUMN 29-30; 23PP; ENGLISH. The present sequence is that of toluene ortho-monooxygenase subunit
20	tomA2 encoded by T44457, isolated from Pseudomonas cepacia strain
CC	PR1-23. The Tom gene is present on a large self-transmissable plasmid
ე <u>წ</u>	denoted prom. The entryme is capable of degrading trichloroethylene denoted by hydrardous and literate the amount also the promit is transmissible and
3 8	(102), a maraturus portaria. Ilse prom passini is cambilissame and expressable in other bacteria, thus many bacteria can be denetically
S	altered to constitutively degrade TCE, esp. in bioreactors or
ဥ္	TCE-contaminated environments. P. cepacia PRI-23 contg. pTOM does not
3 5	Heed exceptions chemical inducers and is capable of indictioning under a distance cat of conditions also it does not require an inducer a
88	
ပ္ပတ္တ	
õ	
M B	Similarity 73.0%; Pred. No. 1.9e-38; 5; Conservative 14; Mismatches 10;
ΟŊ	VESPGMVKIDAPDRLTIRRETIEELTGT
Q	
QY	$\alpha$
QQ	63 DLQQIHINLITLSGYIDEDDEQFTLSWKH 91
RESULT	11.7. 2
W98972 ID W	972 W8972 standard; Protein; 90 AA.
됨	10-MAY-1999 (first entry)

 $\alpha$ 

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:::: : | ||: | 100 | 130 VERI-----VHGFIDD 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; N70196
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                    RESULT
                                                                R40815
                a
                                                                             d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷
                                                                                                                                                            the fields of petroleum purification, chemical and drug industries Claim 1; Page 7-19; 35pp; Japanese.

The present sequence encodes Alcaligenes sp. protein PoxC. The present invention also describes PoxB, PoxI, PoxE, PoxF, PoxG, PoxI and PoxI. The proteins are useful in the fields of petroleum purification, chemical industry and drug industry related to the synthesis, conversion and decomposition of aromatic compounds.
         Alcaligenes; PoxR; PoxR, PoxB; PoxC; PoxD; PoxE; PoxF; PoxG; PoxH; PoxI; aromatic; oxidative; petroleum purification; chemical industry;
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New encoding an aromatic cpd. oxidative decompsn. enzyme - useful in
                                                                                                                                                                                                                                                                                                                                    2 SNVFIAFQANEDSRPIVDAIVADNPRAVVVESPGMVKIDAPDRLTIRRETIEELTGTRFD 61
                                                                                                                                                                                                                                                                                                                                                   3 ANVXIALQNNDDTRPIIEAIAEANPLAVVSQFPAMVKIDAPGRLTIVRELVADKLGRDMD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 DSRPIVDAIVADNP-----RAVVVESPGMVKIDAPDRLJIRRETIEELT-----GTRFD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCA-2 can be prepared commercially for use in the preparation of
drug for the treatment of hyperlipidaemia.
                                                                                                                                                                                                                                                                                                                .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .410 /label= cytrochrome P-450 containing activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 410;
                                                                                                                                                                                                                                                                                    57.0%; Score 257; DB 1; Length 90; 57.5%; Pred. No. 7e-26; Live 16; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cytochrome P450 SCA-2 gene - from Streptomyces carbophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 12-14; 18pp; Japanese.
R51368 showes a protein having cytochrome P-450 activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1994 (first entry)
Protein containing Cytochrome P450 SCA-2 activity.
Cytochrome P450 SCA-2; Streptomyces carbophilus;
treatment of hyperlipidaemia; drug preparation.
Streptomyces carbophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.0%; Score 67.5;
31.2%; Pred. No. 1.1
tive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyperlipidaemia
                                                                                                                                                                                                                                                                                                                                                                                                  62 LQQLQVNLITLSGHIDEDDDEFTLSWS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R51368 standard; Protein; 410 AA.
 Alcaligenes sp. protein PoxC
                                                                                                                                                                                                                                                                                     Query Match 57.09
Best Local Similarity 57.55
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 LOQLQVNLITLSGHIDE 78
                                                                                                25-JUL-1997; JP-200625.
(TOFU ) TONEN CORP.
WPI; 99-197820/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-AUG-1992; 229969.
28-AUG-1992; JP-229969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  useful in treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SANY ) SANKYO CO LID.
                                                                                     25-JUL-1997; 200625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 94-128679/16.
N-PSDB; Q61452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 AA;
                                                  Alcaligenes sp.
                                                                                                                                       N-PSDB; X18867
                                                                        16-FEB-1999.
                                                            J11042088-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J06070780-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                     drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
R51368
δλ
                                                                                                                                                                                                                                                                                                                                                                                                            qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Сp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
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Claim 1; Page 15-23; 43pp; English.
The gene (047743) encodes a spike protein (R40815) which is lacking the transmembrane and cytoplasmic anchor regions of native IBV.
The truncated spike protein can be used to vaccinate fowl, esp poultry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                934 VFIHFSYTPDSFVNVTAIVGECVKPANASQYAIVPANGRGIFIQVNGSYYITARDMYMPR 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----DNPRAVVVESPGMVKIDAPDRLTIR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Fig 1; Zipp; Bnglish.

Proteins encoded by IBV strains M41, D1466, D207 or D274are claimed together with the genes that encode them, and the gene that encodes a protein from IBV strain H120. In addition, a peptide is claimed, characterised in that it comprises at least one of the regions in which the AA sequences of the IBV strains M41 and M42 are different, esp. the region between AAS 5 and 70 and/or between AAS 190 and 301.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New gene coding for protein of infectious bronchitis viruses -useful in prodn. of peptide or protein for vaccination of poultry against the viruses.
                                                       Tring 1994 (first entry)
Truncated IBV spike protein.
Truncated ibv spike protein.
Infectious bronchitis virus; IBV; spike protein; transmembrane; cytoplasmic; anchor; vaccine; poultry; fowl.
Infectious bronchitis virus strain M41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding truncated spike protein of infectious bronchitis
virus - used to express protein to protect fowl, esp. poultry,
against viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.4%; Score 65; DB 1; Length 1093; 26.7%; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 RETIEEL-TGTRFDLQQLQVNLITLSGHIDEDD----DEFTLSWS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1991 (first entry)
Sequence of a region of the S1 protein of infectious
bronchitis virus (IBV) strain M41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Mismatches
                                                                                                                                                                                                                                                         01-SEP-1993.
17-FEB-1993; 003123.
19-FEB-1992; GB-003509.
(BRIE-) BRITISH TECHNOLOGY GROUP LTD.
Skinner MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Poultry vaccine; antigen; immunogen.
Infectious bronchitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DUIN) DUPHAR INT RES BV.
Niesters HGM, Van der Zeijst BAM; WPI; 87-130709/19.
R40815 standard; Protein; 1093 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P70137 standard; protein; 1162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 VFIAFQANEDSRPIVDAIVA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-MAY-1987.
28-OCT-1986; 201884.
31-OCT-1985; NL-002975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from IBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1093 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 93-275023/35.
N-PSDB; Q47743.
```

3;

Matches

g

δ

gs

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threonine synthase, threonine deaminase or S-adenosylmethionine synthase. The invention also relates to the construction of a chimaric gene encoding all or a portion of the biosynthetic pathway enzyme, in sense or antisense orientation, where expression of the chimeric gene results in production of altered levels of the enzyme in a transformed host cell. Overexpression or reduction of enzyme expression of genes encoding the amino acid biosynthetic pathway enzymes in crop plants such as corn, soybean and wheat can be used to alter levels of the amino acids in human food and animal feed. Transformed host cells can also be used to identify compounds that sequence 394 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SNVFIAFQANED-----SRPIVD---AIVADNPRAVVVESPGMVKIDAPDRLTIRRET 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 70-71; 98pp; English.

This is the amino acid sequence of a full-length wheat
S-adenosylmethionine synthetase, as deduced from a cDNA contig (see
8.767185) obtained from kernel, leaf, seedling and root cDNA clones.
The wheat enzyme shows sequence similarity to the barley enzyme.

The invention relates to new isolated nucleic acid fragments (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New plant amino acid biosynthetic enzymes, DNA and chimeric genes encode: dihydropicolinate reductase; diaminopimelate epimerase; threonine synthase; threonine deaminase; S-adenosylmethionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X07168-85) encoding plant enzymes (see W97727-44) that catalyse steps in the biosynthesis of lysine, threonine, methionine, cysteine and isoleucine from aspartate, the enzyme being selected from dihydropicolinate reductase, diaminopimelate epimerase,
                                            Wheat S-adenosylmethionine synthetase.
S-Adenosylmethionine synthetase; wheat; amino acid; lysine;
threonine; methionine; cysteine; isoleucine; transgenic plant;
crop improvement; food; feedstuff.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :| || :| || :| 335 ILKLVKENFDFRPGMISINLDLKKGGNRFIKTAAYGHFGRDDADFT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 IEELTGTRFDLQ--QLQVNL-----ITLSGHIDEDDDEFT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Falco SC, Hitz WD, Kinney AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 64.5; DI
Pred. No. 2.5;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "encoded by CAR"
                                                                                                                                                                                                                                                                           /note= "encoded by AAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "encoded by CGY"
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "encoded by ACS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DUPO ) DU PONT DE NEMOURS & CO E I.
Abell LM, Allen SM, Falco SC, Hitz W
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W80988 standard; Protein; 292 AA.
                                                                                                                                                                                                                                                                                                                                            /note= "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.3%;
30.2%;
             21-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1998; U11692.
12-JUN-1997; US-049443.
06-JUN-1997; US-048771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rafalski JA, Thorpe CJ;
WPI; 99-070263/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
'-has 32; Conserv?
                                                                                                                                                                                                                                                                                                          Misc_difference 150
                                                                                                                                                                                                                                                                                                                                                                          Misc_difference 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc_difference 290
                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc_difference 282
                                                                                                                                                                                                                                             Misc_difference 93
                                                                                                                                                                            Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; X07185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W80988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W80988
             NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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                                                                                                                                                                         3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant turkey herpes viruses contg, foreign DNA encoding a cytokine - useful in vaccines to protect against Marek's disease virus and other avian viruses.

Example 4: Page 185-188; 249pp; English.

Example 4: Page 185-188; 249pp; English.

Recombinant turkey herpes virus (TH) which comprise a foreign DNA sequence encoding a cytokine inserted into a Khol site within an ECORI #9 genomic fragment, where the cytokine can be expressed in host cells infected with the virus can be used in vaccines to protect turkeys against avian viruses. The recombinant viruses can be used for immunising birds against infectious bronchitis virus (IBV), infectious laryngotracheitis virus (ILV) and Newcastle disease (MDV) infectious laryngotracheitis virus (ILV) and Newcastle disease virus (NDV). They may also be used in multivalent vaccines to protect against two or more of these avian viruses. This sequence is the major neutralsing antigen of infectious bronchits virus and commenced in the recombinant vaccines.
                                                                                                                                                                                                                                                                                            934 VFIHFSYTPDSFVNVTAIVGFCVKPANASQYAIVPANGRGIFIQVNGSYYITARDMYMPR 993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                      -DNPRAVVVESPGMVKIDAPDRLTIR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----DNPRAVVVESPGMVKIDAPDRLTIR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MARA-1997 (first entry)
Major neutralising antigen of infectious bronchitis virus.
Major neutralising antigen of infectious bronchitis virus.
Turkey herpes Virus; recombinant virus; vaccine; prophylaxis; immunisation; avian virus; infectious bornchitis virus; infectious bursal disease virus; Newcastle disease virus; Marek's disease virus; infectious laryngotracheitis virus; IBDV; IDDV; MDV; MDV; ILV.
Infectious pronchitis virus (Massachusetts strain).
                                                                                                                                                                      20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                     DB 1; Length 1162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 1162;
                                                                                                                                                                      46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  994 AITAGDIVTLTSCQANYVSVNKTVITTFVDNDFDFNDELSKWWN 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         994 AITAGDIVTLISCQANYVSVNKTVITTEVDNDDFDFNDELSKWWN 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 RETIEEL-TGTRFDLQQLQVNLITLSGHIDEDD----DEFTLSWS 88
                                                                                                                                                                                                                                                                                                                                                            49 RETIEEL-TGTRFDLQQLQVNLITLSGHIDEDD----DEFTLSWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wild MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.4%; Score 65; DB 1
26.7%; Pred. No. 9.3;
live 11; Mismatches
                                                                                                                                                                  11; Mismatches
                                                                                                     Score 65;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Singer PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W06829 standard; Protein; 1162 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W97744 standard; Protein; 394 AA.
W97744;
                                                                                                     14.48;
26.78;
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                                                                                                                                                                                                                            4 VFIAFQANEDSRPIVDAIVA---
                                                                                                                                                           28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-1996.
09-ANG-1995; U10245.
09-ANG-1994; US-288065.
22-DEC-1994; US-362240.
SYTR ) SYNTRO CORP.
COChran MD. JUNKER DE,
WPI; 96-139689/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Junker DE,
1162 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                Best Local Similarity
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      Sequence
                                                                                                  Query Match
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9

34; Indels 31; Gaps

RESULT W97744

qq

AC B

g

DB 1; Length 394;

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N-PSDB; T99141
                                                                                                                                                                                                                                                                                                                                         J09313186-A
                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W34541;
                                                                                                                                                                                                                                                                             W34540;
                                                                                                                                                                                                                                         RESULT 10
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                                                                                                   Matches
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                                                                                                                                                                                                                                                      W34540
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                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                        ;;
                                                                                                                                               New human TSC-22-like protein - for treatment, prevention and diagnosis of developmental, respiratory and neurological disorders claim 18; Fig 2; 65pp; English.

Claim 18; Fig 2; 65pp; English.

This is the amino acid sequence of the human TSC-22-like protein-2 (HT2D-2) used in the method of the invention used in the treatment, and diagnosis of developmental respiratory and neurological disorders. Other uses for HT2L-2 include generation of antibodies and screening for specific binding agents (potential therapeutics). HT2L-2 and its fragments are used as antisense/ribozyme therapeutics, for detecting and quantifying gene expression (as probes and primers in standard hybridisation and amplification assays), for isolating related sequences and for chromosome mapping. Antibodies are used directly as therapeutic antagonists, as immunoassay reagents for diagnosis or isolate HT22L-2 from natural sources.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; N60679.
Artificial infectious bronchitis virus spike protein - and corresp. DMA molecules useful as probes for the infection Disclosure; Page 6-11; 44pp; English.
The patentors claim a sequence which codes for (1) the spike protein
                                                                                                                                                                                                                                                                                                                                                                                                                                13 DSRPIVDAIVADNPRAVVVESPGMVKIDAPDRLTIRRETIEELIGIRFDLQQLQVNLIIL 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----DPFGAVAAQKFSLAH---SMLAI 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUL-1991 (first entry)
Sequence of the S1 signal and S1 and S2 polypeptides of the spike
Amino acid sequence of the human TSC-22-like protein-2. Human; TSC-22-like protein-2; HT22L-2; respiratory disorder; neurological disorder; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Poultry; infectious disease; diagnosis; probe; virus-typing.
                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                        21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Infectious bronchitis virus (IBV) Beaudette strain.
Key
                                                                                                                                                                                                                                                                                                                                                                                                       13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              14.2%; Score 64; Di 24.6%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Binns MM, Boursnell MEG, Brown TDK; WPI; 86-278819/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P60720 standard; Protein; 1162 AA.
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/label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-JUN-1985; GB-015678.
(NATR ) NATIONAL RES DEV CORP.
(BINN/) BINNS M M.
                                                                                                                                                                                                                                                                                                                                                                                                                                              19. .537
/label= S1
538. .1162
/label= S2
                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 24.6'
Matches 17; Conservative
                                                                                                   (INCY-) INCYTE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-MAR-1986, G00181.
29-MAR-1985; GB-008265.
                                                                          04-MAY-1998; U09122.
05-MAY-1997; US-851190.
                                                                                                                Goli SK, Hillman JL;
WPI; 99-034708/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGHLDSDDD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHIDEDDD
                                                                                                                                        N-PSDB; V68643
                                        Homo sapiens.
W09850425-A2.
                                                                12-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W08605806-A
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                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide
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This sequence represents the S-adenosylmethionine synthase 1 (saml) protein. The DNA encoding this sequence may be used in producing plants which are resistant to alkaline soil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               saml; barley; alkali resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sam2; barley; alkali resistant plant.
                                                                                                                                                                                                                                                                                          283 SGAYIARQAAKSIIASGLARRCIVQISYAIGVPEPLSVFVDSYGTGKI--PDR-----E 334
precursor; (2) the S1 signal plus the S1 polypeptide; (3) the S1 polypeptide; or (4) the S1 polypeptide plus the S2 polypeptide, pref. of IBV Beaudette, M41 or 6/82 strain.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                            ----DNPRAVVVESPGMVKIDAPDRLTIR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SNVFIAFQANED-----SRPIVD---AIVADNPRAVVVESPGMVKIDAPDRLTIRRET
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S-adenosyl-methionine synthase gene - useful in producing plants
resistant to alkaline soil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31;
                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 394;
                                                                                                                                                      ; Score 64; DB 1; Length 1162;
; Pred. No. 13;
11; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Indels
                                                                                                                                                                                                                                                                                                                                                                                           335 ILKLVKENFDFRPGMITINLDLKKGGNRFIKTAAYGHFGRDDADFT 380
                                                                                                                                                                                                                                                                                                                                                             49 RETI-BELIGTRFDLQQLQVNLITLSGHIDEDD----DEFTLSWS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 IEELTGTRFDLQ--QLQVNL------ITLSGHIDEDDDEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.1%; Score 63.5; DB 1; 30.2%; Pred. No. 3.4; Live 9; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-1998 (first entry)
S-adenosylmethionine synthase 1.
S-adenosylmethionine synthase 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S-adenosylmethionine synthase 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W34540 standard; protein; 394 AA
                                                                                                                                                                                                                                                            4 VFIAFQANEDSRPIVDAIVA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAY-1996; JP-133406.
(NIOC) NIPPON OIL CO LTD.
WPI; 98-080077/08.
                                                                                                                                                                                                         28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-1997.
28-MAY-1996; 133406.
28-MAY-1996; JP-133406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1996; 133406
                                                                                1162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
Les 32; Conserv
                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hordeum vulgare.
J09313186-A.
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O'Keefe DP, Omer C!
WPI; 91-102077/14.
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                                                                                                                                                                                                                                                 DE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fertility
                                                                                                                                      Sequence
                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                17
                                                                                                                                                                                                                                                                    135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                            R61118
     Qy
                                                                                                                                                                                                                             qq
                                                                                                                                                                                                                                                 ŏŏ
                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                      ;9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
Claim 2; Page 6-7; 13pp; Japanese.
This sequence represents the S-adenosylmethionine synthase 2 (sam2) protein. The DNA encoding this sequence may be used in producing plants which are resistant to alkaline soil.
Sequence 394 AA;
                                                                                                                                                                                                                                                                                                                                                                    resistant to alkaline soil
Claim 3; Page 7-8; 13pp; Japanese.
This sequence represents the S-adenosylmethionine synthase 3 (sam3)
protein. The DNA encoding this sequence may be used in producing plants
which are resistant to alkaline soil.
                                                                                                                                                                                                                                                                   sam3; barley; alkali resistant plant.
                                                                                                                                  283 SGAYIARQAAKSIIASGLARRCIVQISYAIGVPEPLSVFVDSYGTGKI--PDR-----E 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 SGAYIARQAAKSIIASGLARRCIVQISYAIGVPEPLSVFVDSYGTGKI--PDR-----E 334
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNVFIAFQANED-----SRPIVD---ALVADNPRAVVVESPGMVKIDAPDRLITRRET 51
                                                                                                               2 SNVFIAFQANED-----SRPIVD---AIVADNPRAVVVESPGMVKIDAPDRLTIRRET 51
                                                                                                                                                                                                                                                                                                                                                          S-adenosyl-methionine synthase gene - useful in producing plants
                                                                                            31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Indels 31;
                                                                         Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 394;
                                                                                           34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytochrome enzyme P450SU1.
Cytochrome P450; P450SU1; P450SU2; herbicide resistance.
                                                                                                                                                                    84
                                                                                                                                                      52 IEELTGTRFDLQ--QLQVNL------ITLSGHIDEDDDEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 IEELIGIREDLQ--QLQVNL------ITLSGHIDEDDDEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harder PA, Leto KJ, Lichtner FT, Odell JT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 63.5; DB
Pred. No. 3.4;
9; Mismatches
                                                                     Score 63.5; DE Pred. No. 3.4;
                                                                                           Mismatches
                                                                                                                                                                                                                                                        S-adenosylmethionine synthase 3. S-adenosylmethionine synthase 3;
                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
                                                                                           6
                                                                                                                                                                                                                           W34542 standard; protein; 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R11349 standard; Protein; 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DUPO ) DU PONT DE NEMOURS CO.
                                                                       14.18;
30.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.1%;
30.2%;
                                                                                                                                                                                                                                                                                                                            (NIOC ) NIPPON OIL CO LID. WPI; 98-080077/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                               26-MAR-1998 (first entry)
                                                                                           32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-SEP-1989; US-405605.
12-JAN-1990; US-464499.
23-AUG-1990; US-569781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptomyces griseolus.
                                                                                                                                                                                                                                                                                                         28-MAY-1996; 133406.
28-MAY-1996; JP-133406.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-MAR-1991.
27-AUG-1990; U04785.
                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      394 AA;
                                                                                                                                                                                                                                                                             vulgare.
                                                                                                                                                                                                                                                                                                                                                  N-PSDB; T99143
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Simi
Matches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9103561-A.
                                                                                                                                                                                                                                                                                      J09313186-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-1991
                                                                                                                                                                                                                                                                                                  09-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                             Hordeum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dean C,
                                                                                                                                                                                                                                     W34542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R11349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                         335
                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R11349
ID R1
                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                 W34542
  84 55 55 58
88 55 55 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding cytochrome P450 enzymes - and electron donating iron-sulphur proteins, used to confer herbicide resistance to plants and microorganisms.

Claim 13; page 151; 224pp; English.

This cytochrome P450 enzyme, P450sUl is expressed alongside the iron sulphur protein Res. B, by a DNA sequence contained in a recombinant plasmid. Host Streptomyces species are transformed with the plasmid and are used to coat a plant seed to transform the plant. The res-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 DALVADNPR-AVVVESP-GMVKIDAPDRLTIRRETIEELTGTRFDLQQLQVNLITLSGHI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeast cytochrome oxidase subunit IV presequence; cox IV; cox II; wheat cytochrome oxidase subunit II; chimeric gene; unedited mitochondrial gene; transgenic plant; male-sterile plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 32-33; 64pp; French.

The COX II from wheat is fused to codons 1-62 of the subunit IV of yeast cytochrome oxidase. The COX IV transfer sequence directs the COX II to mitochondria. "Editing" the COX II gene results in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic plant contg non-edited mitochondrial gene - linked to
transfer sequence, able to impart male sterility without altering
other characteristics, also antisense constructs for restoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        changes to 16 amino acids, compared to the unedited version. The unedited COX II is preferred because it results in male-sterility by inhibiting pollen production in transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07\text{-APR-}1995 (first entry) Yeast presequence COX IV-wheat COX II (unedited) fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.7%; Score 62; DB 1; Length 322; 32.1%; Pred. No. 4.1; tive 12; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .62
/note= "yeast COX IV amino acids 1-62"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                             ultant transformants are resistant to herbicides.
See also Q11127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 62.5;
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= COX_II
/note= "unedited version"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric Saccharomyces cerevisiae. Chimeric Triticum sp.
Romesser JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R61118 standard; Protein; 322 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-AUG-1994.
115-FEB-1994, F00162.
115-FEB-1993; FR-001650.
(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.9%;
35.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transgene; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63. 322
CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Araya A, Mouras A;
WPI; 94-279755/34.
N-PSDB; 070275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      406 AA;
                                                     N-PSDB; 011126.
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5
58 NVTLIRRVNEDLLEPVSCDLSDDMPWSACPHPRCVPRRCVIPCQSFVVTDVDYFSFQPDR 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-chain of human granulocyte-macrophage CSF receptor - used for screening agonists and antagonists of human GM-CSF, e.g. for diagnosing myeloid leukamists of human GM-CSF, e.g. for Claim 2, Page 15-18, 20pp, English.

The nucleic acid encoding the human GM-CSF beta-chain is isolated from a cDNA library prepd. from poly(A)+ RNA from TF-1 cells. The high affinity human GM-CSF receptor (Kd < 1 nM) can be used for screening candidate GM-CSF agonists and antagonists e.g. for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---PLGTRL-----TVTLLYQHVQPPEPRDLQISTDQDHFLLTWS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 LTIRRETIEELEGTRFDLQQLQVNLITLSGH------IDEDDDEFTLSWS 88
                                                                                                                                                                                 17-MAY-1992 (first entry)
Sequence of beta-chain of a human granulocyte-macrophage colony stimulating factor (GM-CSF) receptor Agonist; antagonist; myeloid leukaemia; therapy; screening; diagnosis; granulocyte-macrophage colony stimulating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.7%; Score 62; DB 1; Length 897; 24.6%; Pred. No. 16; tive 9; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 NVFIAFQANEDSRPIVDAIVADN-------PRAVVVESPGMVKIDA-
                                                                                                                                                                                                                                                                                                             1. .17
/label= signal
58 . 60
/label= glycosylation
191 . 193
/label= as above
346 . 348
/label= as above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SCHE ) SCHERING CORP.
Hayasahida K. Kitamura T, Miyajima A,
WPI; 92-064947/08.
N-PSDB; Q21453.
                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                  288 EIRGINHAFIPIVVEAVILKDYAD 311
                                                                                                                                                                      R20982 standard; Protein; 897 AA.
                                                             54 ELIGIRFDLQQLQVNLITLSGHID 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating myeloid leukaemias.
Sequence 897 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 24.69
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-FEB-1992.
16-JUL-1991; U04846.
18-JUL-1990; US-554745.
                                                                                                                                                                                                                                                                                                                                                                      modified_site
                                                                                                                                                                                                                                                                                                                                          modified_site
                                                                                                                                                                                                                                                                                                                                                                                                       modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                      W09201788-A.
                                                                                                                                                                                                                                                                                                               peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118
                                                                                                                                         RESULT
R20982
                                                                                                                                                                       Dp
                                                             δ
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Search completed: September 26, 2000, 20:11:44 Job time: 10368 sec

# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

September 26, 2000, 20:30:02; Search time 58.11 Seconds (without alignments) 47.462 Million cell updates/sec Run on:

US-09-430-029-4 451 1 MSNVFIAFQANEDSRPIVDA.....ITLSGHIDEDDDEFTLSWSH 89 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

85661 seqs, 30989116 residues Searched:

Total number of hits satisfying chosen parameters:

85661

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_38:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Description	P19731 pseudomonas	pseudomona	synechocys	Q06561 caenorhabdi	P27356 methylosinu	-	homo sap		P12651 avian infec	P34643 caenorhabdi	-	Q61414 mus musculu	P11223 avian infec	005494 bacillus su			P49612 pisum sativ		P39694 bacillus su	_				ıo		7	P53520 proteus mir	P47465 mycoplasma	P43281 lycopersico		98 bacillus s	P55624 rhizobium s	3351
CHTARMOC		ID	DMPM_PSESP	TMOD_PSEME	MUS2_SYNY3	UN52_CAEEL	MMOB_METTR	CHMU_ERWHE	ELF1_HUMAN	METK_MESCR	VGL2_IBVM	YOQ5_CAEEL	CORA_ECOLI	K1CO_MOUSE	VGL2_IBVB	YDHC_BACSU	METK_HORVU	DCDA_ECOLI	METK_PEA	YFA4_YEAST	CME1_BACSU	CPXE_STRGO	YQY1_CAEEL	YOOG_BPT4	METL_PETCR	METK_POPDE	ELF1_MOUSE	- 1	PMFD_PROMI	Y223_MYCGE	METL_LYCES	NIFN_ANASP		Y4QC_RHISN	PAF1_YEAST
		DB	Т	Н	П	Н	Н	Н	Н	Н	Н	Н	Н	Н	1	Н	П	7	Н	<del></del> 1	Н	H	1	-	П	<del>.  </del>	П	_	Н	Н	H	Н	Н	Н	Н
		Match Length	90	102	822	2481	138	181	619	392	1162	1232	316	452	1162	224	394	420	366	828	205	405	964	82	145	395	612	897	254	411	393	444	543	583	445
ф	Query	Match	4	7.	'n.	14.7	4	4	4	4	4	4	₹.	₹.	14.2	•	14.1	4		4	ω.	13.9	m.		e .	ص	w.	13.7	ω.	m	3	æ.	ω.	۳.	ω.
		Score	247	122	9	66.5	99	99	9	65.5	65	9	64.5	64.5	64	63.5	63.5	63.5	63	63	62.5	62.5	62.5	62	62	62	62	62	61.5	61.5	61	61	61		60.5
	Result	No.	1	2	m	4	5	9	7	∞ .	on ;	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

	POSIZE AVIAN INFECTOR								
ULK1_HUMAN VGL2_IBVD2	VGL2_IBV6	TREB_EMENI	METK_PETCR	KAPR_CAEEL	SUCC_AQUAE	FTSZ_HAEIN	FRUA_STRMU	CBBR_RHORU	METK_MUSAC
	-	-	Н	Н	Н	Н	Н	Н	Н
1050	1163	748	234	376	385	421	1423	298	393
13.4	13.4	13.2	13.1	13.1	13.1	13.1	13.1	13.0	13.0
60.5	59.5	59.5	59	59	59	59	23	58.5	58.5
34 35	36	38	36	40	41	42	43	44	45

#### ALIGNMENTS

a

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SEQUENCE FROM N.A. MEDLINE; 93339574.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNC-52
                            RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UN52_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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0
                                                                                              Gaps
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                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SNVFIAFQANEDSRPIVDAIVADNP-RAVVVES-PGMVKIDAPDRLTIRRETIEELTGTR 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SNVFIAFQANEDSRPIVDAIVADNPRAVVVESPGMVKIDAPDRLTIRRETIEELIGTRFD 61
                                                                                                                                         3 SLYXIAFQDNDNARYVVEAIIQDNPHAVVQHHPAMIRIEAEKRLEIRRETVEENLGRAWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yen K.-M., Karl M.R., Blatt L.M., Simon M.J., Winter R.B.,
Fausset P.R., Lu H.S., Harcourt A.A., Chen K.K.;
"Cloning and characterization of a Pseudomonas mendocina KR1 gene
Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase;
NADP; Flavoprotein; FAD; Iron; Plasmid; 3D-structure.
SEQUENCE 90 AA; 10491 MW; 32B3A5FB72664AED CRC64;
                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cluster encoding toluene-4-monooxygenase.";
-1 BUNCTION: HYDROXYLATES TOLUENE TO FORM P-CRESOL.
-1 COFACTOR: FAD; REQUIRES FE(+2) FOR ACTIVITY.
-1 FIRST STEP IN TOLUENE DESCRAPATION.
-1 SUBUNIT: THE MALITCOMPONENT ENZYME TOLUENE-4-MONOOXYGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aromatic hydrocarbons catabolism; Oxidoreductase; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 102;
                                                                    Length 90;
                                                                  Query Match 54.8%; Score 247; DB 1; Length 90 Best Local Similarity 51.1%; Pred. No. 5.3e-20; Matches 45; Conservative 21; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                   01-NoV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
TOLUENE-4-MONOOXYGENASE SYSTEM PROTEIN D (EC 1.14.13.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E5E4283F8E2904B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.1%; Score 122; DB 1; 32.5%; Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                           102 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 1-21.
                                                                                                                                                                              62 LQQLQVNLITLSGHIDEDDDEFTLSWSH 89
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 FDLQQLQVNLITLSGHIDEDDDE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 AA; 11487 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M65106; AAA26002.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monooxygenase; FAD; Iron.
INIT_MET 0 0
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                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas mendocina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 91358306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas.
                                                                                                                                                                                                                                                                        TMOD_PSEME Q00459;
                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=KR1
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE: 97061201.
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 DSRPIVDAIVADNP--RAVVVESPGMVKIDAPDRLTI-RRETIE-----ELTGTRFDLQQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BASEMENT MEMBRANE PROTEOGLYCAN PRECURSOR (PERLECAN HOMOLOG).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rP (POTENTIAL).
78AE7942F777F721 CRC64;
                                                                                                                                                                        MUTSB OR MUTS2 OR SLL1772.
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chrococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00486; DNA_MISMATCH_REPAIR_2; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 69; DB 1;
Pred. No. 8.6;
                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
   822 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2481 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            822 AA; 90669 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.3%;
36.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D90908; BAA17670.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00488; MutS_C; 1. PFAM; PF01713; Smr; 1.
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   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                      MUTS2 PROTEIN.
MUS2_SYNY3
P73625;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
SEQUENCE
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                                                                              Contraction of the color process and the mandmailed basement memorane heparan color solidate proteoglycan."

1. Sulfate proteoglycan."

2. I-FUNCTION: PROBABLE ROLE IN MYOFILAMENT ASSEMBLY AND/OR ATTACHMENT OF THE MYOFILAMENT LATTICE TO THE CELL MEMBRANE. UNC-52 MAY BE AN EXTRACELLULAR MACHOR FOR INTEGRIN RECEPTORS IN MUSCLE.

2. EXTRACELLULAR LOCATION: EXTRACELLULAR MATRIX.

2. I-SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.

3. CONTRACTIVE PRODUCTS: UNC-52 PRODUCES AT LEAST THREE POLYPEPTIDES:

4. ALTESNEE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANE OF ALL CONTRACTILE TISSUES: IT IS CONCENTRATED OVER MUSCLE DENSE BODIES

3. CONTRACTILE TISSUES: IT IS CONCENTRATED OVER MUSCLE DENSE BODIES

4. SIMILARITY: CONTAINS 3 LDL-RECEPTOR CLASS A DOMAINS.

5. I-SIMILARITY: CONTAINS 1 LIMMUNOGLOBUIN-LIKE C2-TYPE DOMAINS.

5. SIMILARITY: CONTAINS 2 LAMININ BGF-LIKE DOMAINS.

6. SIMILARITY: TO PERLECAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00047; ig; 16.

PFAM; PF00052; laminin_B; 2.

PFAM; PF00053; laminin_B; 2.

PFAM; PF00057; lallercept_a; 3.

R PROSITE; PS001209; LDGRA_1; 3.

R PROSITE; PS01209; LDGRA_1; 3.

R PROSITE; PS01209; LDGRA_1; 3.

R PROSITE; PS01246; LDGRA_1; MEMBRANE PROTEOGLYCAN.

R PROSITE; PS01246; LDGRA_1; MEMBRANE PROTEOGLYCAN.
Rogalski T.M., Williams B.D., Mullen G.P., Moerman D.G.; "Products of the unc-52 gene in Caenorhabditis elegans are homologous to the core protein of the mammalian basement membrane heparan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEJUNE C2-TYPE DOMAIN 1.

LDI-RECEPTOR CLASS A 1.

LDI-RECEPTOR CLASS A 3.

LDI-RECEPTOR CLASS A 3.

LDI-RECEPTOR CLASS A 3.

LDI-RECEPTOR CLASS A 3.

IG-LIKE C2-TYPE DOMAIN 2.

LAMININ BGF-LIKE 1 (INCOMPLETE).

LAMININ BGF-LIKE 2 (N-TERMINAL).

LAMININ BGF-LIKE 2 (N-TERMINAL).

LAMININ BGF-LIKE 3 (INCOMPLETE).

LAMININ BGF-LIKE 4 (N-TERMINAL).

LAMININ BGF-LIKE 5.

LAMININ BGF-LIKE 6.

LAMININ BGF-LIKE 7.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 6.

IG-LIKE C2-TYPE DOMAIN 7.

IG-LIKE C2-TYPE DOMAIN 10.

IG-LIKE C2-TYPE DOMAIN 11.

IG-LIKE C2-TYPE DOMAIN 11.

IG-LIKE C2-TYPE DOMAIN 11.

IG-LIKE C2-TYPE DOMAIN 11.

IG-LIKE C2-TYPE DOMAIN 12.

IG-LIKE C2-TYPE DOMAIN 12.

IG-LIKE C2-TYPE DOMAIN 11.

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IG-LIKE C2-TYPE DOMAIN 13.

IG-LIKE C2-TYPE DOMAIN 11.
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1133
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1887
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PFAM; PF00047;
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   RANGE OF THE STATE OF THE STATE
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IG-LIKE C2-TYPE DOMAIN 15.  IG-LIKE C2-TYPE DOMAIN 16. BY SIMILARITY. BY SUMILARITY. BY SIMILARITY. BY SIMILARI	tch 14.7%; Score 66.5; DB 1; Length 2481; 21; Conservative 14; Mismatches 24; Indels 15; Gaps 21; Conservative 14; Mismatches 24; Indels 15; Gaps PIVDAIVADNPRAVVESFGMVKIDAPDRITIRRETIEELTGTRFDLQQLQVN 68   :	METTR  MANDB_METTR  P27356;  P27 Last sequence update)  P1-AUG-1992 (Rel. 23, Last sequence update)  METHANE MONOXYGENASE REGULATORY PROTEIN B.  MANDB.  MANDB.  MADDLIN: Proteobacteria; alpha subdivision; Rhizobiaceae group;  Methylosytaceae; Methylosinus.  P26UENCE FROM N.A.  MEDLINE: 91251762.  Cardy D.L.N. Laidler V., Salmond G.P.C., Murrell J.C.;  MADLOCHAR analysis of the methane monooxygenase (MMO) gene cluster of Methylosinus trichosporium OB3b.";  MOI. Microbiol. 5:335-342(1991).
2347 2436 2436 114 161 174 183 202 224 225 268 970 970 982 1001 1000 1000 1000 1100 1100 1100 11	tch al Similarity 28.4%; Pred 21; Conservative 14; M PIVDAIVADNPRAVVESPGMVKIDAPD   :       :            PTINRPVESNPARVIVKSPIRPIIDPAE LITLSGHIDEDDDE 82 :   ::        FRRVSGQLNEDADE 1642	METTR  MODE_METTR  MODE_METTR  P27356; P23, Created) P27405-1992 (Rel. 23, Last sequence P27405-1992 (Rel. 23, Last annotath P27406-1992 (
2267 2354 666 166 1156 1156 1160 2233 2233 2233 2233 2233 2233 2233 22	atch 21 Similarity 21; Conserv PIVDAIVADNERAN   :       PTINEPVESNEARV LITLSGHIDEDDDE :   :       FRRVSGQLNEDADE	METTR S 6; 1992 (Rel 16-1992 (Rel 16-1992 (Rel 16-1992 (Rel 10-1992 (R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xia T., Song J., Zhao G., Aldrich H., Jensen R.A.;
"The aroQ-encoded monofunctional chorismate mutase (CM-F) protein is a periplasmic enzyme in Erwinia herbicola.";
J. Bacteriol. 175:4729-4737(1993).
-!- FUNCTION: MAX PRQUESTER WITH CYCLOHEXADIENYL DEHYDRATASE AND PERHAPS AN AMINOTRANEFRASE TO FORM PHENYLAIANINE OR PHENYLPYRUVAIE FOR SOME AS YET UNKNOWN FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNVFIAFQANEDSRPIVDAIVAD------NPRAVVVESPGMVKIDAPDRLITRRETI 52
FUNCTION: THE B PROTEIN ACTS AS A REGULATOR OF ELECTRON FLOW THROUGH THE SOLUBLE MMO COMPLEX, SWITCHING THE ENLYME FROM AN OXIDASE TO A HYDROXYLASE IN THE PRESENCE OF THE SUBSTRATE. SUBUNIT: M.TRICHOSPORTUM HAS TWO FORMS OF METHANE MONOOXYGENASE, A SOLUBLE AND A MEMBRANE-BOUND TYPE. THE SOLUBLE TYPE CONSISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
MONOFUNCTIONAL CHORISMATE MUTASE PRECURSOR (EC 5.4.99.5) (CM-F).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.6%; Score 66; DB 1; Length 138; 25.5%; Pred. No. 2.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          B8FB8731DF525E82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: CHORISMATE = PREPHENATE. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EELIGTRFDLQQLQVNLITLSGHIDEDDDEFTLS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 21-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBCELLULAR LOCATION: PERIPLASMIC.
                                                                                             A SOLUBLE AND A MEMBRANE-BOUND TYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M95628; AAA73360.1; -. PFAM: PF01817; Chorismate_mut; 1. Isomerase; Periplasmic; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                              Oxidoreductase; Monooxygenase.
SEQUENCE 138 AA; 14883 MW;
                                                                                                                                                                                                                                                                                                                                                                 EMBL; X55394; CAA39070.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                     PIR; $15209; $15209.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ATCC 33243;
MEDLINE; 93328677.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHMU_ERWHE P42517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Erwinia.
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Matches 2
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                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: TRANSCRIPTION FACTOR THAT APPEARS TO BE REQUIRED FOR THE T-CELL-RECEPTOR-MEDIATED TRANS ACTIVATION OF HIV-2 GENE EXPRESSION. BINDS SPECIFICALLY TO TWO PURINE-RICH MOTIFS IN THE HIV-2 ENGANCER. ELF-1 BINDS TO THE UNDERPHOSPHORYLATED FORM OF RB. MAY INTERACT WITH OTHER TRANSCRIPTION FACTORS IN ORDER TO REGULATE
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 93262492.

Wang C.Y., Petryniak B., Thompson C.B., Kaelin W.G., Leiden J.M.;

"Requiation of the Ets-related transcription factor Elf-1 by binding
to the retinoblastoma protein.";

Science 260:1330-1335(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A novel Ets-related transcription factor, Elf-1, binds to human minimunodeficiency virus type 2 regulatory elements that are required for inducible trans activation in T cells.", virol. 66:5890-5897(1992).
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PFAM; PF00178; Ets; 1.
PRAM: PF00178; EtsDOMAIN.
PROSITE; PS00346; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS0061; ETS_DOMAIN_2; 1.
Nuclear protein; Transcription regulation; Activator; DNA-binding.
DOMAIN 775 80 POLY-ASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 92407962.
Leiden J.M., Wang C.Y., Petryniak B., Markovitz D.M., Nabel G.J.,
Thompson C.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                    10;
                                                                                                                                                                                                                                                       86
  MONOFUNCTIONAL CHORISMATE MUTASE 5F8F77C0D1E2542E CRC64;
                                                                                                                                                                                                                       39 IDAPDRLTIRRETIEELTGTRFDLQQLQVNLTT-----LSGHIDEDDDEFTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1993 (Rel. 27, Created)
1-OCT-1993 (Rel. 27, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ETS-RELATED TRANSCRIPTION FACTOR ELF-1 (E74-LIKE FACTOR 1).
                                                                                                             Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catarrhini; Hominidae; Homo.
                                                                                                                                                                 17; Indels
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                                                                                                                DB 1;
                                                                                                             Score 66; DB :
Pred. No. 2.9;
                                                                                                                                                                                                                                                                                                                                                                                                                   619 AA
                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: NUCLEAR. SIMILARITY: BELONGS TO THE ETS FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                              11;
     181
20299 MW;
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67455 MW;
                                                                                                          14.6%;
29.6%;
                                                                                                                                                                    16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A43361; A43361.
21 1
181 AA;
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TRANSFAC; T01113; -.
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                                                                                                          Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   ELF1_HUMAN
P32519;
                         SEQUENCE
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                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHIONINE AND ATP (BY SIMILARITY).
-1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)0 = ORTHOPHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           281 SGAYIARQAAKSIVAAGLARRCIVQISYAIGVAEPLSVFVDTYGTGKISDKDILKIVKET 340
                                           Gaps
                                                                        SNVFIAFQAN--EDSRPIVDAIVADNPRAVVVESPGMVKIDAPDRLIIRRETIEELIGIR 59
                                                                                                          NDLVFEFASNVMEDERQLGDPAIF -- PAVIVEHVPGADILNSYAGLACVEEPNDMITESS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNVFIAFQANED-----SRPIVD---AIVADNPRAVVVESPGMVKIDAPDRLIIRRET 51
                                                                                                                                                                                                                                                                                                                                                                                                 Mesembryanthemum crystallinum (Common ice plant).
Eukaryota; Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Caryophyllidae; Caryophyllales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Michalowski C.B., Bohnert H.J.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P04384; IXRC.
PRAM; PF00438; S-AdoMet_synt; 1.
PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
Transferase; One-carbon metabolism: Multigene family; AIP-binding.
NP_BIND
                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 FDFRPG-----MIANNLDLLRGGNRYLKTAAYGHFGRDDADFTWEVVKPLKW 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.5%; Score 65.5; DB 1; Length 392; 29.2%; Pred. No. 8.4; Live 9; Mismatches 38; Indels 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 IEELTGTRFDLQQLQVNLITLS------GHIDEDDDEFT-----LSW
       DB 1; Length 619;
                                         Indels
                                                                                                                                                                                                                                                                                                       15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL).
ATP (POTENTIAL).
D13C2CD03757165A CRC64;
                                       34;
                                                                                                                                                                                                                                                                             392 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
                    Pred. No. 13;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
       Score 66;
                                                                                                                                              FDLQQLQVNLITLSGHIDEDDDEFTLS 86
                                                                                                                                                                                 LDVAEEEI------1DDDDDDITLT 84
                                                                                                                                                                                                                                                                             PRT;
       14.
24.18; Fr.
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     14.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Aizoaceae; Mesembryanthemum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U79767; AAB38500.1; -.
                                     21; Conservative
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Query Match
Best Local Similarity
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Best Local Similarity
Matches 33; Conserv
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P93254;
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                                     Matches
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PRT: 1162 AA

STANDARD;

VGL2\_IBVM

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                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 87021475.
Niesters H.G.M., Lenstra J.A., Spaan W.J.M., Zijderveld A.J.,
Bleumink-Pluym N.M.C., Hong F., van Scharrenburg G.J.M.,
"The peplomer protein sequence of the M41 strain of coronavirus IBV
and its comparison with Beaudette strains.";
                                                                                                                                                                                              Virus Res. 5:253-263(1986).
-!- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
                                                                          Avian infectious bronchitis virus (strain M41) (IBV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
         01-ocr-1989 (Rel. 12, Created)
01-ocr-1989 (Rel. 12, Last sequence update)
15-UUL-1999 (Rel. 138, Last annotation update)
E2 GIXCOPROTEIN PRECRESOR (SPIKE GIXCOPROTEIN) (PEPLOMER PROTEIN)
[CONTAINS: SPIKE PROTEIN S1; SPIKE PROTEIN S2].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3C9CC70938492DDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           3lycoprotein; Envelope protein; Transmembrane; Signal.
SIGNAL
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SPIKE PROTEIN S1.
SPIKE PROTEIN S2.
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EMBL; A24863; CAA01736.1; -.
PIR; S07421.
PFAM; PF01560; COFONA.
PFAM; PF01601; COFONA.S1; 1.
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1038
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1162
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        01-0CT-1989
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STRAIN-K12
               CORA_ECOLI
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               This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation — the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3,
                                                                                                                                                                                                                                                                                                                                                                 Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latrelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sins M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              472 VVDALLVWQLLEIMVQQHG--RVTGPDVATLLTNASEELGEKTGISSNGTSESGSKFEAK 529
                                                                         934 VEIHESYTPDSFVNVTAIVGFCVKPANASQYAIVPANGRGIFIQVNGSYYITARDMYMPR 993
                            Gaps
                                                   4 VFIAFQANEDSRPIVDAIVA-------DNPRAVVVESPGMVKIDAPDRLTIR 48
                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TGTRFDLQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
                           20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 65; DB 1; Length 1232; Pred. No. 37;
DB 1; Length 1162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Indels
                          46; Indels
                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
HYPOTHETICAL 134.9 KDA PROTEIN ZK512.5 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6DFC35D664AA8D6A CRC64;
                                                                                                                  49 RETIEEL-TGTRFDLQQLQVNLITLSGHIDEDD----DEFTLSWS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 IVDAIVADNPRAVVVESPGMVKIDAPDRLTIRRETIEEL-
                                                                                                                                                                                          PRT; 1232 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Mismatches
                          11; Mismatches
 14.4%; Score 65;
              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ll protein.
1232 AA; 134923 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.48; 25.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z22177; CAA80146.1; -.
              26.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WORMPEP; ZK512.5; CE00411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Conservative
                          28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: | | | ||:|
E-RFNKYLLGGHINE 543
                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 QLQVNLITLSGHIDE 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S40766.
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              Similarity
                                                                                                                                                                                                                                                                                                                                           STRAIN-BRISTOL N2; MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S40766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical
SEQUENCE 12
                                                                                                                                                                                          YOQ5_CAEEL
P34643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local &
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               Best Local
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=KIZ ' MG165;
STRAIN=KIZ ' MG165;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes ";
Science 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      a new
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: PLAYS A ROLE IN THE TRANSPORT OF MAGNESIUM AND COBALT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 93347969.
Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
"Analysis of the Escherichia coli genome. III. DNA sequence of the region from 87.2 to 89.2 minutes.";
Nucleic Acids Res. 21:3391-3398(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                             of
                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE; 93300795.
Smith K.L., Banks J.L., Snavely M.D., Maguire M.E.;
"Sequence and topology of the CorA magnesium transport systems salmonella typhimurium and Escherichia coli. Identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SL -> RP (IN REF. 1 AND 3).
G -> A (IN REF. 1).
CC3B1B736EE36A53 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                  01-A0G-1992 (Rel. 23, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Magnesium; Cobalt; Transmembrane; Transport.
316 AA
                                                                                                                                                 MAGNESIUM AND COBALT TRANSPORT PROTEIN CORA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.3%; Score 64.5; D 28.6%; Pred. No. 8.2; tive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      class of transport protein.";
J. Biol. Chem. 268:14071-14080(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000457; AAC76819.1; -. PIR; S30743; S30706; S30706. ECOGNE; ECI1463; CORA. PFAM; PF01544; COTA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36589 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L11042; AAB59046.1; -. EMBL; L02122; AAD15038.1; -. EMBL; M87049; AAA67612.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 28.63
Matches 20; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303
316 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138:197-200(1994).
FUNCTION: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBRILLAR KERATIN: I (ACIDIC; 40-55 KDA) [K9 TO K20] AND II (NEUTRAL TO BASIC; 56-70 KDA) [K1 TO K8]. BOTH A BASIC AND AN ACIDIC KERATIN ARE REQUIRED FOR FILAMENT ASSEMBLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Gaps
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --RETI 52
                                                                                                                                                                                                                                                                                                                                           "The complete sequence of the gene encoding mouse cytokeratin 15.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coil; Heptad repeat pattern; Keratin.
                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIÎ: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ---LVEPDDDERLRVQSELGQSL-ATRPELEDIEA----
                                                                                                                                                                                                                                         Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
KERATIN, TYPE I CYTOSKELETAL 15 (CYTOKERATIN 15) (K15) (CK 15).
KRILS OR KRII-15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQANEDSRPIVDAIVADNPRAVV-VESPGMV----KIDAPDRLTIR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-SER.
C431310A7BB408FD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 DELTLARTDLEMQIEQLNEELAYLKKNHEEEMKEFS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EELTGTRFDL ----QQLQVNLITLSGHIDEDDDEFT 84
                                                                                                                            452 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 64.5;
Pred. No. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKER 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAIL.
COIL 1A.
LINKER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-GLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COIL 1B.
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                            Nozaki M., Mori M., Matsushiro A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Intermediate filament; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.3%;
26.0%;
                                                                                                                                                                                                                                                                                              STRAIN=129/SV; TISSUE=LIVER; MEDLINE; 94171037.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D16313; BAA03821.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:96689; KRT1-15.
PFAM; PF00038; filament; 1.
PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                           STANDARD;
                                                                                                                                                                                                                          Mus musculus (Mouse).
EESQPLVNAVWID--
                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                          72 LSGHIDEDDD 81
                                                     -SARFFEDDD 70
                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
407
98
134
153
265
265
265
421
452
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                                                                                                                           K1CO_MOUSE
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                             'Cloning and sequencing of the gene encoding the spike protein of the
                                                                                                                                                                                                                                                         "Comparison of the spike precursor sequences of coronavirus IBV strains M41 and 6/82 with that of IBV Beaudette."; J. Gen. Virol. 67:2882-2931(1986).
i- FUNCTION: THE PEPLOMER PROTEIN MEDIATES THE BINDING OF VIRIONS
                                                                                               Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                 01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PEPLOMER PROTEIN)
                                                                                                                                                                                                                                                                                                      TO THE HOST CELL RECEPTOR AND IS INVOLVED IN MEMBRANE FUSION.
                                                                                      Avian infectious bronchitis virus (strain Beaudette) (IBV).
                                                                                                                                                      Binns M.M., Boursnell M.E.G., Cavanagh D., Pappind D.J.C., Brown T.D.K.,
                                                                                                                                                                                                                                               Binns M.M., Boursnell M.E.G., Tomley F.M., Brown D.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Envelope protein; Transmembrane; Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPIKE PROTEIN S1.
SPIKE PROTEIN S1.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN DINB-PHOB INTERGENIC REGION.
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Sadaie Y., Yata K., Fujita M., Sagai H., Itaya M., Kasahara Y.,
Ogasawara N.;
"Nucleotide sequence and analysis of the phoB-rrnE-groESL region of
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Microbiology 143:1861-1866(1997).
-!- SIMILARITY: BELONGS TO THE GNTR FAMILY OF TRANSCRIPTIONAL
REGULATORS.
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sin; Transcription regulation; DNA-binding.
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5C41A9E1553B592D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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283 SGAYTARQAAKSIIASGLARRCIVQISYAIGVPEPLSVFVDSYGTGKI--PDR-----E 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -! - CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)0 = ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare (Barley).
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mori S., Takizawa R., Nakanishi H.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                                                                                                             01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
S-ADENOSYLMETHIONINE SYNTHETASE 1 (EC 2.5.1.6) (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mori S., Takizawa R.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
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394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - PATHWAY: ACTIVATED METHYL CYCLE.
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                                                                                          34, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 285-322 FROM N.A.
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30.28;
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STANDARD;
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Best Local Simi
Matches 32;
                                                                                          01-OCT-1996
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HERE AND DESCRIPTION OF THE PROPERTY OF THE PR
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lyis bade Blank (nsbto)

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 26, 2000, 20:28:52; Search time 92.32 Seconds (without alignments) 66.841 Million cell updates/sec Run on:

US-09-430-029-4 451 1 MSNVFIAFQANEDSRPIVDA.....IILSGHIDEDDDEFTLSWSH 89 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

225878 Total number of hits satisfying chosen parameters:

225878 seqs, 69334122 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL\_12:\*

1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_human:\*
6: sp\_namman:\*
7: sp\_mhc:\*; sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\* sp\_organelle:\*
sp\_phage:\*
sp\_plant:\*
sp\_rodent:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		æ			COLUMN TO COLUMN	577		
Result		Query						
No.	Score	Match	Match Length DB	DB	ID	-	Description	cion
-	354	78.5	68	7	030591	) 	030591 P	hurkholderi
7	346	76.7	89	7	052571			pseudomonas
m	326	72.3	97	7	O9ZNP5			COMAMONAS t
7	257	57.0	90	7	084960			ralstonia s
2	247	54.8	06	7	052172			pseudomonas
9	243	53.9	91	7	052163			pseudomonas
7	233	51.7	68	7	032430			acinetobact
8	232	51.4	8	7	043980			acinetobact
σ	114	25.3	110	7	087801			pseudomonas
10	111	24.6	147	7	P95411			pseudomonas
11	110	24.4	104	7	051942			burkholderi
12	105	23.3	105	7	069181			alcalidenes
13	06	20.0	101	7	Q9ZET4			xanthobacte
14	84	18.6	104	7	007071			burkholderi
15	83.5	18.5	862	7	9M8X60			streptomyce
16	77	17.1	1684	4	075218		075218	homo sapien
17	77	17.1	3830	4	Q9Y6H4			homo sapien
18	77	17.1	3859	4	Q9Y631			homo sapien
19	70.5	15.6	174	Н	028973			archaeoglob

059831 streptomyce Q9xtd2 caenorhabdi 018263 caenorhabdi Q9xt15 caenorhabdi 030028 archaeodi		4	006118 methylocyst 000876 renibacteri 09x6r4 aeromonas p 027443 methanobact 054298 streptomyoe	amycol macaca zea ma macaca	V99914 Macaca Lasc 036185 plautia sta Q63128 rattus norv P76578 escherichia
2 059831 5 09xTD2 5 018263 5 09xTD2 1 030028	2 P73736 5 O76870 2 Q92HS9 12 Q66178			2 052820 7 Q95517 8 Q95513 7 Q95513	2 0361 1 0631 P7657
410 2295 2482 3375	263 263 281 1153	1159 352 395 983	138 557 690 139 1541	4077 166 274 354	941 941 1653
15.0 14.7 14.7 14.7	4444	14.4 14.2 14.2	44466	 	
67.5 66.5 66.5 66.5	655 655 655 655 655 655 655 655 655 655	65 64 63 5	63 63 62.5 62.5	62 62 62 62 62 62 62	5555 666 666
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#### ALIGNMENTS

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54.8%; Score 247;
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SEQUENCE 90 AA; 10519 MW;
                                                                                                                                                    novel kinetic properties.",
Microbiology 144:0-0(0).
EMBL; AFOZGOES; AAC32454.1,
HSSP: P19731, 1HQI.
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=P35X / NCBI 9869;
MEDLINE; 95129877.
                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P35X.";
Gene 151:29-36(1994)
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 50; Conserv
                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas.
                                                                            Ralstonia.
                                                                                                             STRAIN-E2;
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Q52172;
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Q52172
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Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSNVFIAFQANEDSRPIVDAIVADNPRAVVVESPGMVKIDAPDRLTIRRETIEELTGTRF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOHNSON G.R., OLSEN R.H.;
"Nucleotide sequence analysis of genes encoding a toluene/Denzene-2-monooxygenase from Pseudomonas sp. strain JS150.";
Appl. Environ. Microbiol. 61:3336-3346(1995).
EMBL; L40033; AAA88458.1; -.
                                                                                                                                                                                                                                            1 MSNVFIAFQANEDSRPIVDAIVADNPRAVVVESPGMVKIDAPDRLTIRRETIEELTGTRF 60
                                                                                                                                                                                                                                                         TOLUENE/BENZENE-2-MONOOXYGENASE (TBMA-TMMF) GENES, COMPLETE CDS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=TA441;
MEDLINE; 99018839.
ARAI H., AKAHIRA S., OHISHI T., MAEDA M., KUDO T.;
"Adaptation of Comamonas testosteroni TA441 to utilize phenol:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organization and regulation of the genes involved in phenol degradation.";
                                                                                                                                                                                                Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.3%; Score 326; DB 2; Length 97; 69.3%; Pred. No. 1.2e-26;
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                                                                                                                                                                                                                      15; Indels
                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                Query Match 76.7%; Score 346; DB 2; Best Local Similarity 75.3%; Pred. No. 9.3e-29; Matches 67; Conservative 7; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MICTODIOLOGY 144:2895-2903(1998).
EMBL; AB006479; BAA34171.1; -.
HSSP; P19731; 1HQI.
SEQUENCE 97 AA; 10728 MW; 47CD2246 CRC32;
                                                                                                                                                      HSSP; P19731; 1HQI.
SEQUENCE 89 AA; 10029 MW; F54D09A2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90 AA.
                                                                                                                                                                                                                                                                                                                                                                    97 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; Mismatches
                                                                                                                                                                                                                                                                                        61 DLQQLQVNLITLSGHIDEDDDEFTLSWSH 89
                                                                                                                                                                                                                                                                                                     DLQQLHVNLVTLSGHIDEDDDQLTLSWQH 89
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ELQQIQINLVTLSGHVDEDDDEFSLSWN 96
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                                                                                                                                                                                                                                                                                                                                                                                                                           PHENOL HYDROXYLASE COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61; Conservative
                                Pseudomonas sp.
Bacteria, Proteobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 61; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                 SEQUENCE FROM N.A.
                                                                           STRAIN=JS150;
MEDLINE; 96035667
          TBMA-TMMF)
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084960
ID 08
AC 08
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Q9ZNP5
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SIMILARITY).
-!- PATHWAY: FIRST STEP OF PHENOL BIODEGRADATION.
-!- SUBUNIT: THE MULTCOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED BY P0, P1, P2, P3, P4 AND P5 POLYPEPTIDES.
EMBL; X79063; CAA55662.1; -
HSSP; P19731; 1HQI.
                                                                                                                                                                                                                                                                                                                                                                                                  N.;
Ralstonia eutropha strain E2 exhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 ANVXIALQNNDDTRPILEAIAEANPLAVVSQFPAMVKIDAPGRLTIVRELVADKLGRDWD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 931298//.
NG L.C., SHINGLER V., SZE C.C., POH C.L.;
"Cloning and sequences of the first eight genes of the chromosomally encoded (methyl) phenol degradation pathway from Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SNVFIAFQANEDSRPIVDAIVADNPRAVVVESPGMVKIDAPDRLTIRRETIEELTGTRFD 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: FAD FLAVOPROTEIN, AND REQUIRES FE(+2) FOR ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase;
                                                                                                                                                                     Ralstonia sp. E2.
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57.0%; Score 257; DB 2; Length 90; 57.5%; Pred. No. 1.3e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1999 (TrEMBLrel. 12, Last annotation update)
PHENOL HYDROXIASE P2 PROTEIN (EC 1.14.13.7)
(PHENOL 2-MONOCXYGENASE P2 COMPONENT).
01-NOV-1998 (TrEMBLrel. 08, Created)
U-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PHENOL HYDROXYLASE COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D9015E61 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8B0F5684 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 LQQLQVNLITLSGHIDEDDDEFTLSWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 LQEIHLNLISLSGNIDETDEAFTLHWS
                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 98361023.
HINO S., WATANABE K., TAKAHASHI
"Phenol hydroxylase cloned from
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Length 90;

DB 2;

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Best Local

Matches

952163

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2 SNVFIAFQANEDSRPIVDALVADNPRAVVVESPGMVKIDAPDRLITRRETIEELIGIRFD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKVYLALQDNDTSRYIIEAIEQDNPQATIQYLPAMIRVESTGELVVRAETVSEKLGQNWD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 96154937.

EHRT S., SCHIRMER F., HILLEN W.;

Genetic organization, nucleotide sequence and regulation of
expression of genes encoding phenol hydroxylase and catechol 1,2-
dioxygenase in Acinetobacter calcoaceticus NCIBB250.";

MOL MACIOCODIO.";

EMBL; 236909; CAA85382.1;

EMBL; 236909; CAA85382.1;

ENSP; P19731; 1HQI.

SEQUENCE 89 AA; 10136 MW; AA99E933 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 SNVFIAFQANEDSRPIVDAIVADNPRAVVVESPGMVKIDAPDRLTIRRETIEELTGTRFD
                                                                                                                                                                                MEDLINE; 98005684.

HORINOUCHI M., KASUGA K., NOJIRI H., YAMANE H., OMORI T.;
HORINOUCHI M., KASUGA K., NOJIRI H., YAMANE H., OMORI T.;
Cloning and characterization of genes encoding an enzyme which
axidizes dimethyl sulfide in Acinetobacter sp. strain 20B.";
FEMS Microbiol. Lett. 155:99-105(1997).

EMBL; D85083; BAA23332.1;
HSSP; P19731; 1HQI.
SEQUENCE 89 AA; 10135 MW; A50444FF CRC32;
                                                            Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PHENCLHYDROXYLASE COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 233; DB 2;
Pred. No. 3.9e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.4%; Score 232; DB 2;
46.0%; Pred. No. 4.9e-17;
iive 21; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 LOQLQVNLITLSGHIDEDDDEFTLSWS 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                       Moraxellaceae; Acinetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                              51.7%;
46.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moraxellaceae; Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acinetobacter calcoaceticus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                          Acinetobacter sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-NCIB8250;
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ID 06
AC 06
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                                                                                               2 SNVFIAFQANEDSRPIVDAIVADNPRAVVVESPGMVKIDAPDRLIIRREIIRELIGIRFD 61
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
-!- PATHWAY: FIRST STEP OF PHENOL BIODEGRADATION.
-!- SUBUNIT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED.
-!- SUBUNIT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED.
-!- SUBUNIT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED.
-!- ROBOTION OF AND PS POLYPEPTIDES.
-!- FORMED PROPERTY 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- COFACTOR: FAD FLAVOPROTEIN, AND REQUIRES FE(+2) FOR ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: PHENOL + NADPH + O(2) = CATECHOL + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas putida.
Plasmid pPGH1.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
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HERRMANN H., MUELLER C., SCHMIDI I., MAHNKE J., PETRUSCHKA L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Localization and organization of phenol degradation genes of Pseudomonas putida strain H."; Mol. Gen. Genet. 247:240-246(1995).
-!- FUNCTION: CATABOLIZES PHENOL, AND SOME OF ITS METHYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.9%; Score 243; DB 2; Length 91; 50.0%; Pred. No. 3.7e-18;
Pred. No. 1.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1999 (TrEMBLrel. 12, Last annotation update)
PHENOL HYDROXYLASE P2 PROTEIN (EC 1.14.13.7)
(PHENOL 2-MONOOXYGENASE P2 COMPONENT).
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Last annotation update)
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SEQUENCE 91 AA; 10661 MW; 129B1FDF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                      91 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą.
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                                                                                                                                                                                                                                  63 VQEMLVDVITIGGNIDEDDDREVLEWKN 90
                                                                                                                                                                                                   62 LOOLQVNLITLSGHIDEDDDEFILSWSH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 LQQLQVNLITLSGHIDEDDDEFTLSWSH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                         PRT;
     52.3%; Pic. 20;
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                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                          Similarity
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Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                         Q52163;
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAHNKE K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=H;
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Gaps 61

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9 QANEDSRPIVDAIVADNP-RAVVVESP-GMVKIDAPDRLTIRRETIEELTGTRFDLQQLQ 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alcaligenes eutrophus.
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                         burkholderia pickettii (Pseudomonas pickettii).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
Ralstonia.
                                                                                                                                                                                                                                                                                                                                                                                       Length 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 105;
                                                                                                                                                                                                                    BYRNE A.M., KUKOR J.J., OLSEN R.H.; "Sequence analysis of the gene cluster encoding toluene-3-monooxygenase from Pseudomonas pickettli PKO1."; Gene 154:65-70(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HARKER A.R., AYOUBI P.J.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF065891; AAC77383.1; -
SEQUENCE 105 AA; 11913 MW; 3971DE3F CRC32;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
TOLUBENG-3-MONOOXYGENASE FERREDOXIN PROIEIN.
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07, Last annotation update)
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32.0%; Pred. No. 0.00069;
Live 17; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                         24.4%; Score 110; DB 2; 32.0%; Pred. No. 0.00021;
                                                                                                                                                                                                                                                                                                                                   31CA0AC7 CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                             20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9ZET4;
01-MAY-1999 (TrEMBLrel. 10, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUTATIVE HYDROXYLASE COMPONENT
                                                                                                                                                                                                                                                                                                                                   104 AA; 11703 MW;
                                                                                                                                                                                                                                                                                              EMBL; U04052; AAB09621.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 23.39
Best Local Similarity 32.09
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                     MEDLINE; 95172404.
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                                                                                                                                                                                                                                                                                                                     Monooxygenase.
SEQUENCE 104
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Q9ZET4
ID Q9ZET4
AC Q9ZET4
DT 01-MAY
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                                                                                                                                                                MEDLINE; 98432776.

MEDLINE; 98432776.

BERTONI G., MARTINO M., GALLI E., BARBIERI P.;

BERTONI G., MARTINO M., GALLI E., BARBIERI P.;

Analysis of the gene cluster encoding toluene/o-xylene monooxygenase from Pseudomonas stutzeri OXI.";

Appl. Environ. Microbiol. 64:3626-3632(1998).

EMBL; AJ005663; CAA006657.1; -.

HSSP: P19731: 1HQI.

SEQUENCE IIO AA; 12274 MW; A15B73F3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 RAGELADAVAEAAREDNPGKEIRVDDKRAXLRIDTDDEMIIRRTTIEQALGRPFDMPELE 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=J1104;
KITAXAMA A., SUZUKI E., KAWAKAMI Y., NAGAMUNE T.;
"Gene organization and low regiospecificity in aromatic-ring
hydroxylation of a benzene monocxygenase of Pseudomonas aeruginosa
J1104.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
Pseudomonas
                                                          Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
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Last annotation update)
   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                                      Query Match 25.3%; Score 114; DB 2; L. Best Local Similarity 37.3%; Pred. No. 8.6e-05; Matches 28; Conservative 15; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.6%; Score 111; DB 2; 33.8%; Pred. No. 0.00025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Ferment. Bioeng, 82:421-425(1996).
EMBL, D83068; BAA11764.1; -.
SEQUENCE 147 AA; 16261 MW; 84995200 CRC32;
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Best Local Similarity 33.8%
Matches 25; Conservative
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86 INLSSFAGIIDMDFD 100
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124 INLSSFAGRIQIND 137
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                     TOUD PROTEIN
                                                                                              Seudomonas.
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RESULT 10

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RESULT 11

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Search completed: September 26, 2000, 20:28:54 Job time: 1013 sec
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ZHOU N.Y., CHAN KWO CHION C.K., LEAK D.J.;
"The alkene monooxygenase from Xanthobacter Py2 is closely related aromatic monooxygenase and catalyses aromatic monohydroxylation of
                                                               Bacteria; Proteobacteria; alpha subdivision; Ancylobacter group; Xanthobacter.
                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
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                                                                                                                                                                                                                                             Query Match 20.0%; Score 90; DB 2; Length 101; Best Local Similarity 24.2%; Pred. No. 0.023; Matches 24; Conservative 19; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.6%; Score 84; DB 2; Length 104; 34.3%; Pred. No. 0.098; tive 10; Mismatches 28; Indels
                                                                                                                                                                   benzene, toluene and phenol.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ01209); CAA09914.1;
SEQUENCE 101 AA: 11194 MW; F4F59639 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MA Y., HERSON D.S.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF001356; AAB58743.1; -.
SEQUENCE 104 AA; 11790 MW; 40251740 CRC32;
01-WAY-1999 (TrEMBLrel. 10, Last sequence update) 01-WAY-1999 (TrEMBLrel. 10, Last annotation update) COUPLING/FEFECTOR PROTEIN.
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Last annotation update)
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Last annotation update)
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                                                  Xanthobacter sp. Py2
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Matches 23; Conserv
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01-NOV-1999
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STRAIN=A3(2);
OLIVER K., HARRIS D.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 MD Streptomyces coelicolor A3(2) chromosome.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J., KINASHI H., HOPWOOD D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

Mol. Microbiol. 21:77-96(1996).

SALO49628; CAB40869.1; -.

SEQUENCE 862 AA; 94537 MW; 631192DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 RAVVVESPGMVKIDAPDRLTIRRETIEELTGTRFDLQQLQVNLITLSGHIDEDDDEFTLS 86
                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
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BENTLEY S.D., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Streptomyces coelicolor.
Bacteria; Firmicutes; Ac
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MEDLINE; 97000351.
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Page 6

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein

September 26, 2000, 20:30:04 Run on:

1 MDIPTLKKKLGLKDRYAAMT.......FDGSEDQKNFAAWRGQAIRN 516 US-09-430-029-5 2873 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

85661 segs, 30989116 residues Searched:

85661 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Listing first 45 summaries Post-processing: Minimum Match 08
Maximum Match 1008

SwissProt\_38:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	200456 pseudomonas 200456 pseudomonas 200456 pseudomonas P22869 methylococc P27353 methylosinu 200460 pseudomonas P25659 bovine leuk P06579 bacillus st. 049621 arabidopsis 027232 methanobact P11558 methanobact P11558 methanobact P11558 methanobact P1158 methanobact P15821 homo sapien P37896 lactobacill P32653 streptococc 2010737 haemonchus P52673 saccharomyc P19252 pisum sativ P22543 saccharomyc P19252 pisum sativ P52095 escherichia P14296 manduca sex 211000 heliothis v 219426 caenorhabdi 084211 chlamydia t P47278 mycooplasma 033367 anacystis n P49093 lotus japon Q13489 homo sapien 058721 pyrococcus
SUMMA	DMFN_PSESP TWOA_PSESP MEMA_METCA MEMA_METCA MEMA_METTR POL_BLVJ ANY_BACST MCHALACTH MCRA_METTH MCRA_METTH MCRA_METTH MCRA_METTH MCRA_METTH MCRA_METTH MCRA_METTH MCRA_METTH MCRA_METTH MCRA_METTH MCRA_METTH MCRA_METTH MCRA_METTH OSTE HUAN STRSU ANY_LACE TBUD_BURP! VSA_YEAST ANY_LACE TBUD_BURP! VSA_ZECL! ANY_MENSE AMPN_HELVI GCS1_CAEEL SYL_CHETR GCS1_CAEEL SYL_CHETR GCS1_CAEEL SYL_CAEEL SYL_CAEEL SYL_CAEEL SYL_CAEEL SYL_CAEEL SYL_CAEEL SYR_MANSE ANY_MOSE ANY_MOSE ANY_MOSE GCS1_CAEEL SYR_MXXAA INVZ_DAUCA ASNZ_LOTJA INVZ_DAUCA ASNZ_LOTJA SYR_MANI
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Ouery Match
64.3%; Score 1846.5; DB 1; Length 517;
Best Local Similarity 64.8%; Pred. No. 2.8e-145;
Matches 328; Conservative 63; Mismatches 106; Indels 9;

013683 schizosacch 046863 escherichia P49092 lotus japon P29190 haemonchus 025cb9 rickettsia 005542 gluconobact P21517 escherichia P74007 synechosyst P12341 kluyveromyc P34528 caenorhabdi	
YDY2_SCHPO YGIS_ECOLI ASNI_LOTTA PPCK_HAECO HTPG_RICPR DHET_GLUSU MALZ_ECOLI SPOT_SYNY3 G6PI_KLULA YNG7_CABEL	CYAA_YERPE
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#### ALIGNMENTS

CTIONNEINTO	RESULT 1 DMPN_PSESP DD DMPN_PSESP STANDARD; PRT; 517 AA.	01-FEB-1991 (Rel. 17, Creat 01-FEB-1991 (Rel. 17, Last	15-FEB-2000 (Rel. 39, Last PHENOL HYDROXYLASE P3 PROTE	DMPN OR PHE?	OS Pseudomonas sp. (strain CF600). OG Plasmid pVI150.	OC Bacteria; Proteobacteria. RN (1)	REP SEQUENCE FROM N.A. RX MEDLINE: 91072230.	Nordlund "Complete	multicomponent phenol hydroxylase from Pseudomonas sp.			RC STRAIN≃BH; RA Takeo M., Maeda Y., Okada H., Mivama K Mori K Ike M.	Fujita M.;	-i-	CC DERIVATIVES. P3 IS REQUIRED FOR GROWTH ON PHENOL, AND FOR CC IN VITRO PHENOL, HYDROXYLASE ACTIVITY.	1.	+	CC -:- PATHWAY: FIRST STEP OF PHENOL BIODEGRADATION.	BY PO, Pl, P2, P3, P4 AND P5 POLYPEPTIDES.		CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	use by non-profit institutions as long a		CC or send an email to license@isb-sib.ch).	EMBL; M60276; AAA25942.1; EMBL; D28864; BAA06017.1; PIR; D37831; D37831.	KW Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase; KW NADP; Flavoprotein; FAD; Iron; Plasmid. SO SFOIRENCE 517 AB. 60522 MM. AFEMARDAOFF73780 CRC64.	, m 22000 (mg / t ) 1000 (mg / t)
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                                                                                                                                                                                                                                                                                                                                                                                                                   426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      486
                                                                                                                                                                                                                           306
                                                                                                                                                                                                                                                                                                  246 KFMLEQHEDNVPIIQRWIDKWFWRGYRLTLILIGMMMDYMLPNKVMSWSEAWGVYFEQAGG 305
                                                                                                                                                                                                                                                                                                                                                                   127 EGARIACOMOSIDELRHYQTETHAMSTYNKFFNGFHHSNOWFDRVWYLSVPKSFFEDAYS 186
                                                                                                                                                                                                                                                                                                                                               ALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWLSAK 366
                                                                    QGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGRHFTG 126
                                  65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yen K.-M., Karl M.R., Blatt L.M., Simon M.J., Winter R.B., Fausset P.R., Lu H.S., Harcourt A.A., Chen K.K.; Cloining and characterization of a Pseudomonas mendocina KR1 gene cluster encoding tolunen 4-monocxygenase."; J. Bacteriol. 173:5315-5327(1991).
                   KFLLEQDPDNVP1VQRWIDKWFWRGYRLLTLVAMMMDYMQPKRVMSWRESWEMYAEQNGG
 KKKLGLKDRYAAMTRGLGWETTYQPMDKVFPYDRYEGIKIHDWDKWVDPFRLTMDAYWKY
                                                                                                                                                                                                         SGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIECI
                                                                                                                                                                                                                                                                                                                                                                                                                YPDSFDRYYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKIGARESNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGNKFHFCSDHCKDIFDHEPQKYVQAWLPVHQIHQGNCFPPDADPGAEGFDPLAAVLDYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: HUDROXIALTES TOLDENE TO FORM P-CRESOL.
COCRACTOR: FAD; REQUIRES FE(+2) FOR ACTIVITY.
PATHWAY: FIRST STEP IN TOLUENE DEGRADATION.
SUBDINT: THE MULTICOMPONENT ENZYME TOLUENE-4 MONOOXYGENASE
IS FORMED BY THE TMOA, TWOB, TMOE, TMOE AND TMOF
POLYPEPTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
TOLUENE-4-MONOOXYGENASE SYSTEM PROTEIN A (EC 1.14.13.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 499 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 1-13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIKSGVDNLEYLGSPEHQRWLALKGO 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         487 AVTMGRDNLDFDGSEDQKNFAAWRGQ 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas mendocina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 91358306
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01-AUG-1991 (Rel. 19, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
METHANE MONOOXYGENASE COMPONENT A ALPHA CHAIN (EC 1.14.13.25) (METHANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405
                                                                                                                                                                                                                                                                     EKKLYAVIDAFTONNAFLGVSDARYINALKLFLOGVTPLEYLAHRGFAHVGRHFTGEGAR 130
                                                                                                                                                                                                                                                                                                                                                                      124 NMATFGMMDELRHGOLOLFFPHEYCKKDROFDWAWRAYHSNE-----WAAIAAKHFFDDI 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  401 IPLVGV-PGDDWNIEVFSLEHNGRLYHFGSEVDRWVFQQDPVQYQNHMNIVDRFLAGQIQ 459
                                                                                                                                                                    Gaps
                                                                                                                                                                                                  13 KDRYAAMTRGLGWETTYQPMDKVFP--YDRYEGIKIHDWDKWVDPFRLTMDAYWKYQGEK 70
                                                                                                                                                                                                                                   64
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Methylococcus capsulatus
                                                                                                                                                                                                                                   6 KDWY-ELTRATNWIPSYVIEEQLFPERMSGHMGIPLEKWESYDEPYKISYPEYVSIQREK
                                                                                                                                                                                                                                                                                                   DAGAYSVKAALERAKIYEN-SDPGWISTLKSHYGAIAVGEYAAVTGEGRMARFSKAPGNR
                                                                                                                                                                                                                                                                                                                                                                                                                                       179 ITGRDAISVAIMLTESFETGFTNMQFLGLAADAAEAGDYTFANLISSIQTDESRHAQQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 -EWIIGQFERSLIDLGLDKPWYWDLFLKDIDELHHSYHMGVLDWRTTAWWNPAAGV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 PIEDEMGWLSAKYPDSFDRYYRPRFDHWGE-----QARAGNRFYM---KTLPMLCQTCQ
                                                                                                                                                                                                                                                                                                                                      131 IACQMQSIDELRHYQTETHAMSTYNKFFNGF-----HHSNQWFDRVWYLSVPKSFFEDA
                                                                                                                                                                                                                                                                                                                                                                                                      185 YSS-GPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 ECIKFLLEQDPDNVPIVQRWIDKWFWRGYRLL-TLVAMMMDYMQP--KRVMSWRESWEMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 AEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQ-----AWSTFYGFNAASAFHTWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 -IPEERDWLEEKYPGWNKR-----WGRCWDVITENVLNDRMDLVSPETLPSVCNMSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                406 IPMLFTEPGNPTKIGARESNYLGNKFHFCSDHCKDIFDHEPQKYVQAWLPVHQIHQGNCF
                                                                                                                                                                    63;
                            Aromatic hydrocarbons catabolism; Oxidoreductase; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methylococcus capsulatus.
Bacteria; Proteobacteria; gamma subdivision; Methylococcaceae;
                                                                               16BD8D41BAB63B49 CRC64;
                                                                                                                                                                  Mismatches 244;
                                                                                                                                  DB 1;
                                                                                                                        Score 374.5; DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   485
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Salmond G.P.C.,
gene cluster of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE; 94077176.
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                                                                                                                                                                71;
                                                                             499 AA; 57851 MW;
                                                                                                                               13.0%;
26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stainthorpe A.C., Lees V., "The methane monooxygenase
              EMBL; M65106; AAA25999.1;
                                             Monooxygenase; FAD; Iron.
INIT_MET 0 0
                                                                                                                                                                Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                  Similarity
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Best Local S
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Nature 366:537-543(1993).

-!- FUNCTION: RESPONSIBLE FOR THE INITIAL OXYGENATION OF METHANE TO

--- METHANOTIC IN METHANOTROPHS, IT ALSO CATALYZES THE MONOHYDROXYLATION

METHANOTROPHS, IT ALSO CATALYZES THE MONOHYDROXYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAD(P)(+) + H(2)0.

COFACTOR: BINDS TWO IRON ATOMS.

SUBDILT: M.CAPSULATOS TWO FROM SOFT WETHANE MONOOXYGENASE,
SUBDILT: M.CAPSULATOS HAS TWO FORMS OF METHANE MONOOXYGENASE,
A SOLUBLE AND A MEMBRANE-BOUND TYPE. THE SOLUBLE TYPE CONSISTS
OF THREE COMPONENTS (A, B AND C): PROTEIN A, COMPRISING THREE
CHAINS, IN AM ALPHA-2, BETR-2, GAMMA-2 COMFIGURATION, IS A
NONHEME IRON PROTEIN CONPLAINING AN UNUSUBLA MU-HYDROXO BRIDGE
STRUCTURE AT ITS ACTIVE SITE AND INTERACTS WITH BOTH OXYGEN AND
     Rosenzweig A.C., Frederick C.A., Lippard S.J., Nordlund P.;
"Crystal structure of a becterial non-haem iron hydroxylase that
catalyses the biological oxidation of methane.";
                                                                                                                                                                                                                                                                 METHANOL IN METHANOTROPHS. IT ALSO CAPALYZES THE MONOHYDROXXI
OF A VARIETY OF UNACTIVATED ALKENES, ALICYCLIC, AROMATIC AND
HETEROCYCLIC COMPOUNDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: METHANE + NAD(P)H + O(2) = METHANOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METHANE
RAHAR RAHARA
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22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPFRLTMDAYWKYQGEKEKKLYAVID-AFTQNNAFLGVSDARYINALKLFLQGVTPLEYL 112
                                                                                                                                                                      --SNFLEVGEYNAIAATGMLWDSAQAAEQKNGYLAQVLDEIRH----THQCAYVNYYFAK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                       :|| : | : | :: | :: | :: | 333 KDAKQDAYWAHHDLYLLAYALWPTGFFRLALPDQEEMEWFEANYPGWYD-HYGKIYEEW-
                                                                                                    EQFKLIAKEYARMEAVKDERQFGSLQVALTRLNAGVRV-HPKWNETMKVV------
                                                                                                                                                                                                        NG---FHHSNQWFDR----VWYLSVPKSFFEDAYSSGPFEFLTAVSFSF-----EYVLT
                                                                                                                                                                                                                                                                          NLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIECIKFLLEQDPDNVPIVQRWID
                                                                                                                                                                                                                                                                                                            NPLIVAVTEWAAANGDEITPTVFLSIETDELRHMANGYOTV-VSIANDPASAKYLNTDLN
                                                                                                                                                                                                                                                                                                                                            266 KWFWRGYRLLT-LVAMMMDYMQPKRVMSWRESWEMYA-EQNGGALFKDLARYGIREPKGW
                                                                                                                                                                                                                                                                                                                                                                 QDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWLSAKYPDSFDRYYRPRFDHWG
                                                                                                                                    113 AHRGFAHVGRH----FTG---EGARIACQ-----MOSIDELRHYQTETHAMSTYNKFF--
                                                                                                                                                                                                                                        161 NGQDPAGHNDARRIRIGPLW--KGMKRVFSDGFISG-----DAVECSLNLQLVGEACFI
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                                   97;
   DB 1; Length 527;
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQARAGNRFYMKTLPMLCQTCQIP-----MLFTEPGNPTKI-
                 1.3e-13;
hes 179;
                                 Mismatches
8.9%; Score 254.5; 24.2%; Pred. No. 1.3
                                 65;
                                   Conservative
                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -RARG---
                                 109;
 Query Match
                   Local
                 Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19;
                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 28, Last annotation update)
METHANE MONOOXYGENASE COMPONENT A ALPHA CHAIN (EC 1.14.13.25) (METHANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 FLGVSDARYINALKLFLQGVTPLE----YLAHRGFAHVGRHFTGEGARIACQMQSIDELR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KYHMANETKEOFKVIAKEYARMEAAKDEROFGTLLDGLTRLGAGNKVHPRWGETMKVISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADP; One-carbon metabolism; Iron.
                                                                                                                                                                           subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.3%; Score 211; DB 1; Length 525; 21.0%; Pred. No. 5.2e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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422 -- RESNYLGNKFHFCSDHCKDJFDHEPQKY 449
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                                                                                                                                                              Methylosinus trichosporium.
Bacteria; Proteobacteria; alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; Monooxygenase;
ACT_SITE 151 151 PO
                                                                                                                                                                                      Methylocystaceae; Methylosinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WW.
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                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114
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209
243
246
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                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 MEDLINE; 91251762
                                                                                                                                         HYDROXYLASE)
                                                                                                                                                                                                                      STRAIN=OB3B;
                                                                                                                                                                                                                                                                                                                                                                                                                                 METHANE
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                                                                           MEMA_METTR
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SEQUENCE
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Matches
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                                                                                                          DPDNVPIVQRWIDKWFWRGYRLLT-LVAMMMDYMQPKRVMSWRESWEMYAEQN-GGALFK 310
                                                                                                                                                                                                                                                                                       320 RLGKYGV-ESRVLRDAKRDAYWAHHDL-----ALAAYAMWPLAFARLALPDEEDQAW 370
    ----NQWFDRVWYLSVPKSFFEDAY-SSGPFEF 192
                                        147 H----THQCAFINHYYSKHYHDPAGHNDARRTRAIGPLW--KGMKRVFADGFISRDAVEC 200
                                                                                 193 LIAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIECIKFLLEQ 252
                                                                                                                                                                                                        DPASAKFLNTDLNNAFWTQQKYFTPVLGYLFEYGSKFKVEPWVKTWNRWVSEDWGGIWIG 319
                                                                                                                                                                                                                                               311 DLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTW-----VPTEDEMGW 362
                                                                                                                                                                                                                                                                                                                                  363 LSAKYPDSFDRYYRPRFDHWG----EQARAGNRFYMKTLP-----MLCQTCQIPMLFTEP 413
                                                                                                                                                                                                                                                                                                                                                                      371 FEANYPGWAD-HYGKIFNEWKKLGYEDPKSGFIPYQWLLANGHDVYIDRVSQVPFI---P 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEAR K.-M., KARI M.R., Blatt L.M., Simon M.J., Winter R.B.,
Fausset P.R., Lu H.S., Harcourt A.A., Chen K.K.;
Follohing and characterization of a Pseudomonas mendocina KRI gene
cluster encoding toluene-4-monooxygenase.";
J. Bacteriol. 173:5315-5327(1991).
-I- FUNCTION: HYDROXYIATES TOLUENE TO FORM P-CRESOL.
-I- COPACTON: FIRST STEP IN TOLUENE DEGRADATION.
-I- PATHWAY: FIRST STEP IN TOLUENE DEGRADATION.
-I- SUBUNIT: THE MULTICOMPONENT ENZYME TOLUENE-4-MONOOXYGENASE
IS FORMED BY THE TMOB, TMOB, TMOD, TMOD, TMOE AND TMOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Aromatic hydrocarbons catabolism; Oxidoreductase; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
TOLUENE-4-MONOOXYGENASE SYSTEM PROFFEIN E (EC 1.14.13.~).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              084EE106D06FB5EC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 AA.
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HYQTETHAMSTYNKFFNGFHHS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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INIT_MET
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TMOE_PSEME
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                                                                                                                                              140 ELR---HYQTETHAMS-TYNKFENGFHHSNQWFDRVWYLSVPKSFFEDAYSSGPFEFLTA 195
                                                                       83 QNNAFLGVSDARYINALKLFLQGVTPLEYLAH---RGFAHVGRHFTGEGARIACQMQSID 139
                                  42 WELSPDSPMNLWYKQYRNASPLKHDNWDAFTDPDQLVYRTYNLMQDGQESYVQSLFDQFN 101
82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Gen. Virol. 71:1737-1746(1990).
-!- PTM: SPECIFIC ENTYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
-!- SIMILARITY: VERY STRONG, WITH BOVINE LEUKEMIA VIRUS ENV
POLYPROTEIN FROM OTHER ISOLAIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coulston J., Naif H., Brandon R., Kumar S., Khan S., Daniel R.C.W.,
                                                                                            25 WE-TIYQPMDKVF-PYDRYEGIKIHDWDKWVDPFRLTMDAYWKYQGEKEKKLYAVIDAFT
                                                                                                                                                                                 158 SLRWLTHTAYRTHELSLTYPDAGLGEHERELWEKEPGWOGL-RELME-----KQLTA
                                                                                                                                                                                                                       196 VSFSFEYVLTNL------LEVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIECI
                                                                                                                                                                                                                                                        209 FDWGEAFVSLNLVVKPMIVESIFKPLQQQAWENNDTLLPLLIDSQLKDAERHSRWSKALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; RNA-directed DNA polymerase; Hydrolase; Nuclease;
Endonuclease; Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lavin M.F.; "Molecular cloning and sequencing of an Australian isolate of proviral bovine leukaemia virus DNA: comparison with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retroviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 115; DB 1; Length 852; Pred. No. 0.085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bovine leukemia virus (Australian isolate) (BLV).
Viruses; Retroid viruses; Retroviridae; BLV-HTLV
                                                                                                                                                                                                                                                                                                                                                                                                                             852 AA.
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                                                                                                                                                                                                                                                                                                                   269 KHALE-NPDNHAVIEGWIEKW 288
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18.78;
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                                                                                                                                                                                                                                                                                            247 KFLLEQDPDNVPIVQRWIDKW
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PFAM; PF00552; integrase;
PFAM; PF00075; rnaseH; 1.
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Matches 134; Conservative
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P25059:
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Gaps

32;

Length 326;

5.3%; Score 152; DB 1; Length 32 24.5%; Pred. No. 2.1e-05; ive 34; Mismatches 131; Indels

24.5%;

Conservative

Best\_Local Similarity Matches 64; Conserv

Query Match

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                                                                                                                                                                                                                                                267
                                                                                                                                                                                                                                                                        446 RGAYCLWKDHILDFQAVPAPESAQKGELAGILAGLAA----APPEPLNI-----WVDSKY 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431
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-!- PIM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
-!- SIMILARITY: VERY STRONG, WITH BOVINE LEUKEMIA VIRUS ENV POLYPROTEIN FROM OTHER ISOLARES.
                                         281
                                                                                                                                                48 DWDKWVDPFRLTM-----DAYWKYQGEKEKK-----LYAVIDAFTQNNAFLGVSDARYI
                                      ----SPISLHOLQTVLGDLQWVSRGTPTTRRPLQLLYSSLKGIDDPRAIIHLSPEQQ-
                                                                     --FAHVGRHFTGEGARIAC-QMQSIDELRHY
                                                                                              -----QGIAELRQALSHNARSRYNEQEPLLAYV--HLTRAGSTLVLFQKGAQFPLAYF
                                                                                                                                                                                    170 ---RVWYLSVPKSFFEDAYSSGPFE-----FLTAVSFSFEYVLTNLLFVPFMSGAAY
                                                                                                                                                                                                                393 ELLQLW----PQISSQGIQPPGPWKTLVIRAEVFLTP-QFSPEPIPAALCL--FSDGAAR
                                                                                                                                                                                                                                           NG------DMSTVTFGFSAQSDESRHMTLGIECIKFLLEQDPDNVPIVQRWID-KW
                                                                                                                                                                                                                                                                                                                                                               -----ESWEMYAEQNGGALFK----DLARYGIREPKGWQDACE-----GKDHI
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                                                                                                                            145 QT -----NOWFD-----ETHAMSTYNKFFNGFHHS-----NOWFD----
                                                                                                                                                                                                                                                                                                                                497 LYSLLRTLVLGA----WLOPDPVPSYALLYKSLLRHPAIFVGHVRSHSSASHPIASLNNY
                                                                                                                                                                                                                                                                                                                                                                                                                       334 SHQAWS-----TFYGFNAAS-AFHTWVPTEDEMGWLSAKYPDSFDRYYRPRFD---
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Sagata N., Yasunaga T., Tsuzuku-Kawamura J., Ohishi K., Ogawa Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEC-1998 (Rel. 37, Last annotation update)
POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49);
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BLV-HTLV retroviruses.
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01, Last sequence update)
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Viruses; Retroid viruses; Retroviridae;
                                                                                                                                                                                                                                                                                                     268 FWRGYRLLTLVAMMMDYMQPKRVMSWR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --PGAEG---FDPLAAVLDYYAVTMGRDN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                     NALKLFLOGVTPL-EYLAHRG-
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21-JUL-1986 (Rel.
15-DEC-1998 (Rel.
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P03361;
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SPISLHOLOAVLGDLOWVSRGTPTTRRPLOLLYSSLKRHHDPRAIIQLSPEQ-- 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 OTPLIDNQASPWGLILLILGCOYLQTQALSSYAKPILKYYHNLPKISLDNWIQSSEDPRVQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 ELLQLW----PQISSQGIQPPGPWKTLITRAEVFLTP-QFSPDPIPAALCL--FSDGATG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --TYQPM-----DKVFPYDRYEGIKIH 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 SPTEEORSOCYQALAARLRDLGFQVASEKTSQTPSPVPFLGOMVHEQIVTYQSLPTLQIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DWDKWVDPFRLIM-----DAYWKYQGEKEKK-----LYAVIDAFIQNNAFLGVSDARYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 NALKLFLQGVTPL-EYLAHRG...--FAHVGRHFTGEGARIAC-QMQSIDELRHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---RVWYLSVPKSFFEDAYSSGPFE-----FLTAVSFSFEYVLTNLLFVPFMSGAAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 NG------DMSTVTFGFSAQSDESRHMTLGIECIKFLLEQDPDNVPIVQRWID-KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         446 RGAYCLWKDHLLDFQAVPAPESAQKGELAGLLAG-----LAAAPPEFVNI---WVDSKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       553 VDQLLPLETPEQWHKLTHCNSRALSRWPNPRISAWDPRSPATLCETCQKLNPTGGGKMRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 SHQAWS-----TFYGENAAS-AFHTWVPTEDEMGWLSAKYPDSFDRYYRPRFD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         613 IQRGWAPNHIWQADITHYKYKQFTYALHVFVDTYSGATHASAKRGLTTQTTIEGLLEAIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HWGEQAR----AGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKIGARES-----NYLGNKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----EIHAMSTYNKFFNGFHHS-----NQWFD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     497 LYSLLRILVLGA----WLOPDPVPSYALLYKSLLRHPAIVVGHVRSHSSASHPIASLNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207;
                                                                                                                                                                                                                                                                                               Transferase; RNA-directed DNA polymerase; Hydrolase; Nuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                   95182 MW; A7A63524A18C458D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 0.35; 70; Mismatches 214;
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                        3.7%; Score 107.5; 19.0%; Pred. No. 0.3
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 3.7%
Best Local Similarity 19.0%
Matches 115; Conservative
                                                                                                                                               PIR, A03960; GNLJGB.
HSSP; P04585; IRT1.
PFAM; PF00552; integrase;
PFAM; PF00075; rnaseH; 1.
                                                                                                                           EMBL; K02120; AAA42785.1;
                                                                                                                                                                                                                                                                                                                       Endonuclease; Polyprotein
                                                                                                                                                                                                                                                                                rvt; 1
                                                                                                                                                                                                                                                      PF00665; rve;
                                                                                                                                                                                                                                                                                                                                                   852 AA;
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                                                                                                                                                                                                                                                                           PF00078;
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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DT 15-DE
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                                                                                                                                                                                                                                                                                                                                                                                                     Ihara H., Sasaki T., Tsuboi A., Yamagata H., Tsukagoshi N., Udaka S., "Complete nucleotide sequence of a thermophilic alpha-amylase gene: homology between prokaryotic and eukaryotic alpha-amylases at the
                                                                                                                                                                                                                    Nakajima R., Imanaka T., Aiba S.; "Nucleotide sequence of the Bacillus stearothermophilus alpha-amylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               þλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tsukagoshi N., Iritani S., Sasaki T., Takemura T., Ihara H., Addota Y., Yamagata H., Udaka S.; Tadota S.; T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carmona C., Requadt C.; "Structural genes encoding the thermophilic alpha-amylases of Bacillus stearothermophilus and Bacillus licheniformis."; J. Bacteriol. 166:635-643(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sray G.L., Mainzer S.E., Rey M.W., Lamsa M.H., Kindle K.L.,
ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Glycosidase; Carbohydrate metabolism; Signal. SIGNAL 35 549 ALPHA-AMVIASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-122 FROM N.A., AND SEQUENCE OF 35-48
                                                                        Bacillus stearothermophilus.
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 35-39
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                        Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                                      Bacteriol. 163:401-406(1985).
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PFAM; PF00128; alpha-amylase; 1
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EMBL; X02769; CAA26547.1; --
EMBL; M57457; AAA22227.1; --
EMBL; M13255; AAA22241.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           active sites.";
J. Biochem. 98:95-103(1985).
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PIR; A24549; A24549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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MEDLINE; 86008166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=DY-5;
MEDLINE; 86059211
                                                                                                                                                                                            85234394
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272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGLG--WETTYQPMDKVFPYDRYEGI------KIHDWDKW-----VDPFRLTMDAY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLH1_ARATH STANDARD; PRT; 526 AA.
049621; 022766;
115-JUL-1999 (Rel. 38, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
115-JUL-1999 (Rel. 38, Last annotation update)
115-JUL-1999 (Rel. 38, Last annotation update)
MLO PROTEIN HOMOLOG 1 (ATMLO-HI).
MLO PROTEIN HOMOLOG 2 (ATMLO-HI).
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Embryophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 WKYQGEKEKKLYAVIDAFTQNNAFL--GVSDARYINALKLFLQGVTPLEYLAHRGFAHVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213 RGIGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKSWGKWYVNTTNIDGFRLDAVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 EDAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---AVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGYPCVFYGDYYGIPQYNIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               276 -----TLVA------SWEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 YAEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVP---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 VGKQHAGKVFYDLT--GNR----SDTVT----INSDGWGEF-KVNGGSV-SVWVPRKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 IKF-----EYWSY-----SFFPDWLSDVRSQTGKPLFTVG----EYWSY----
                                                                                                                                                                                                                                                                                                                                                                                                                                            3.6%; Score 104; DB 1; Length 549;
18.3%; Pred. No. 0.39;
tive 43; Mismatches 125; Indels 198;
                                                                                                                                                                                                                  AND 4).
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                                                                 L -> W (IN REF. 3).

L -> S (IN REF. 3).

P -> H (IN REF. 2 AND 3).

A -> T (IN REF. 2 AND 5).

T -> I (IN REF. 4).

S -> N (IN REF. 4).

S -> N (IN REF. 4).

TNI -> RTL (IN REF. 4).

M -> T (IN REF. 2, 3 AND 4).

TNI -> RTL (IN REF. 2, 3 AND 4).

M -> T (IN REF. 2, 3 AND 4).

T -> A (IN REF. 2, 3 AND 3).

T -> N (IN REF. 2 AND 3).

T -> N (IN REF. 2).

S -> C (IN REF. 2).

WS -> RP (IN REF. 2).

B -> G (IN REF. 2).

S -> P (IN REF. 2).

S -> D -> G (IN REF. 2).

S -> P (IN REF. 2).
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                                                        REF.
REF.
                   SIMILARITY.
SIMILARITY.
                                                         NI) A <-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                        Hasegawa A.,
                                                                                                                                                                                                                             Kaplan N., Johnson D., Schutz K., Gnoj L., Hoffman J., Till S., de la Bastide M., Granat S., Hameed A., Gottesman T., Hasegawa A. Shohdy N., Parnell L., Dedhia N., Johnson A.F., Lodhi M., Martienssen R., Chen E.Y., Wilson R., McCombie W.R.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78;
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E -> GTVHTHTHQQ (IN REF. 2).

MISSING (IN REF. 2).
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                                                                                         Panstruga R.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
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8E63C276A71A9768 CRC64;
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EMBL; AC002330; AAC78258.1;
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                                                                                                                                                                                                          STRAIN-CV. COLUMBIA;
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RESULT 10 MCRA\_METTH

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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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CATALYTIC ACTIVITY: REDUCTION OF METHYL-COENZYME M (2-(METHYLTHIO) ETHANESULEONIC ACID) WITH 7-MERCAPTOHEPTANOYLTHEONINE PHOSPHATE TO METHANE AND AN HETERODISULFIDE (CH(3)-S-COM + H-S-HTP = CH(4) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.

BUENELOPMENTAL STRAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.

MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
CONTAINS MOSTLY MCR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstati
the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE: 98037514.

Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Kangale P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Molling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pihl T.D., Sharma S., Reeve J.N., "Growth phase-dependent transcription of the genes that encode the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rospert S., Linder D., Ellermann J., Thauer R.K.;
"Two genetically distinct methyl-coenzyme M reductases in
Methanobacterium thermoautotrophicum strain Marburg and delta H.";
                                                                                                                                                                                                                                                  Methanobacterium thermoautotrophicum.
Archaea; Buryarchaeota; Methanobacteriales; Methanobacteriaceae;
                   02722; 050493;
15-UTL-1998 (Rel. 36, Created)
15-UTL-1998 (Rel. 36, Last sequence update)
15-FBE-2000 (Rel. 39, Last annotation update)
METHYL-COENZYME M REDUCTASE I ALPHA SUBUNIT (EC 1.8.---) (MCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methylteirahydromethanopterin:coenzyme M methyltransferase in Methanobacterium thermoautotrophicum delta H.", J. Bacteriol. 176:6384-6391(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanogenesis; Oxidoreductase; Methylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eur. J. Biochem. 194:871-877(1990).
-!- FUNCTION: THIS ENZYME COMPLEX CATALYZES THE FINAL STEP IMETHANOGENESIS, WHICH IS THE TERMINAL STEP OF ANAEROBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               two methyl coenzyme M reductase isoenzymes and N5-
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TO TWO MOLECULES OF COENZYME
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=DELTA H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
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                                                             17;
                                                                                                                                                                                                      265 YLPVRRARGENEPGGVPF-----GYLADICQSSRVNYEDPVRVSLDVVATGAML 313
                                                                                                                                                                                                                                                        -----WLSAKYPDSFDR 373
                                                                                                                                                                                                                                                                                                                                                        ---MS 292
                                                                                                                                                                                                                                      WRESWEMYAEQNGGALFKDLA---------RYGIREPKGWQDACEGK 330
                                                                                                                                                                                                                                                                                                               --LDVASEVTFYGLEQYEEYPALL --EDQFGGSQRAAVVAAAAGCSTAFATANAQTGLSG 425
                                                                                                                                                                                                                                                                                                                                       YYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKI-GARESNYLGNKFH 432
                                                                                                                                                                                                                                                                                                                                                                                                                  ------PHAARGDAFVFNPLV-----KIAFAD 514
                                                                                     141 LRHYQTETH----AMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFED------AYSSGPF 190
                                                                                                           145 VQEHMVETHPALVADSYVKVFTGNDEIADEIDPAFVIDINKQFPEDQAETLKAEVGDGIW 204
                                                                                                                                     191 EFL---TAVSFSFEYVLT---NLLFVPFMSGAAYN---GDMSTVTFGFSAQSDESRHMTL 241
                                                                                                                                                            OVVRIPTIVSRICDGATTSRWSAMQIGMSMISAYKQAAGEAATGDFAYAAKHAEVIHMGT 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bokranz M., Baeumner G., Allmansberger R., Ankel-Fuchs D., Klein A., "Cloning and characterization of the methyl coenzyme M reductase genes from Methanobacterium thermoautotrophicum.";
J. Bacteriol. 170:568-577(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 98035783.

Ermler U., Grabarse W., Shima S., Goubeaud M., Thauer R.K.;

"Crystal structure of methyl-coenzyme M reductase: the key enzyme of blological methane formathon.";
                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        FCSDHCKDIFDHEPQKYVQAWLPVHQIHQGNCFPPDADPGAEGFDPLAAVLDYYAVTMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1989 (Rel. 12, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
METHYL-COENZYME M REDUCTASE I ALPHA SUBUNIT (EC 1.8.-.-) (MCR I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133)
Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
                                                            Mismatches 178; Indels 118;
                                                                                                                                                                                       242 GIECIKFLLEQDPDNVPIVQRWIDKWFWRGYRLLTLVAMMMDYMQPKRV---
9C414DA3A785E509 CRC64;
                                    1;
                                  Score 103; DB Pred. No. 0.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              549 AA.
                                                                                                                                                                                                                                                                                       DHISHQAWSTFYGFNAASAFHTWVPTEDEMG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            K-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                            54;
60350 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 -----QGEYAGISQA----
                                  3.68;
                                                            85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| || : : ||
DNLVEDFTNVRGEFA 529
                                                                                                                                                                                                                                                                                                                                                                                                                                          DNLDFDGSEDQKNFA 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                Similarity
549 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 88115150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methanobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MCRA_METTM
P11558;
01-OCT-1989 (
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SEQUENCE
                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
FUNCTION: THIS ENZYME COMPLEX CATALYZES THE FINAL STEP IN BETHANOGENESIS. WHICH IS THE TERMINAL STEP OF ANAEROBIC DEGRADATION OF BIOMASS. CATALYTIC ACTIVITY: REDUCTION OF METHYL-COENZYME M (2-(METHYLTHIO)
                                                                                                                                                                                                                                                                                             SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.

BUSUELOPMENTAL STRACE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.

MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
CONTAINS MOSTLY MCR I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              141 LRHYQTETH----AMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFED------AYSSGPF 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 373 ATEVTFYGLEQYEEYPALL--EDQFGGSQRAAVVAAAAGCSTAFATGNAQTGLSGWYLSM 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --PHAARGDAFVFNPLV----KIAFADDNLVF 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 BEL---TAVSFSFEYULT---NLLFVPFMSGAAYN---GDMSTVTFGFSAQSDESRHMTL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CKDIFDHEPQKYVQAWLPVHQIHQGNCFPPDADPGAEGFDPLAAVLDYYAVTMGRDNLDF 497
                                                                                                                    ETHANESULFONIC ACID) WITH 7-MERCAPTOHEPTANOYLTHREONINE PHOSPHATE TO METHANE AND AN HETERODISULFIDE (CH(3)-S-COM + H-S-HTP = CH(4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                       COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY) TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW NICKEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 YLPVRRARGENEPGGVPF-----GYLADICQSSRVNYEDPVRVSLDVVATGAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---LFKDLARYG---IREPKGWQDACEGKDHISHQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methanogenesis; Oxidoreductase; Methylation; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 549;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 GIECIKFLLEQDPDNVPIVQRWIDKWFWRGYRLLTLVAMMMDYMQPKRV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHYLATION.
979ABB4B6CB8622B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293 WRESWEMYAEONGGA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1MRO; 11-NOV-98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      549 AA;
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269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 RGFAHVGRHFTGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --VIDAFTQNNAFLGVSDARYINALKLFLQGVTP-LEYLAH 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----EKKL 74
                                                                                                                                                                                                                                                             Fleischman R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs I., Hedblom E., Cotton M.D., Utterback Tr., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Ghebm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               447 YATRYEQKKGSGKNAEDVQKTVNRVIPQFKVDLQSVLARDITFLKEYTQTFEPHVQYL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 SVPKSFFEDAYSSGPFEFLTAVSFSFEYVLTNLL-FVPFMSGAAYNGDMSTVTFGFSAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538 ----SLFRDRRYSG----LDRISSANQVTLGGTTRFYDIAGEERFNLSAGQIYYLSNSRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 DESRHMTLGIECIKFLLEQDPDNVPIVQRW--IDKWFWRG-YRLLT-----LVAMMMDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---WKISNKWYWRGSYQFDTHTNSTSLANTSLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
ORGANIC SOLVENT TOLERANCE PROTEIN HOMOLOG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 128; Indels 106;
                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                          "Whole-genome random sequencing and assembly of Haemophilus influenzae \operatorname{Rd."};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285 MQPKR---VMSWRESWEMYAEQNGG----ALFKDLARYGIREPKGWQDA 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.3%; Score 95; DB 1; Length 782; 20.1%; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OUTER MEMBRANE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E73C8A5786B02D1B CRC64;
                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
OKGANIC SOLVENT TOLERANCE PROTEIN HOMOLOG PRECURSOR.
IMP OR OSTA OR HI0730.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FPYDRYE----GIKIHDWDKWVDPFRLTMDAYWKYQGEK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCIENCE CONTROL OF THE B.COLT HOMOLOG.
-!- SUMILARITY: STRONG, TO THE B.COLT HOMOLOG.
782 AA.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32756; AAC22389.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 20.19 tes 70; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Outer membrane; Signal.
                                                                                                                               Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            782 AA;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                           STRAIN=RD / KW20;
MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                          Venter J.C.;
                                                                                                                                                                       Haemophilus.
OSTA_HAEIN
P44846;
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MEDLINE; 91308093.

A MEDLINE; 91308093.

A MEDLINE; 91308093.

C Ship of the solution of the 
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                                                                                                                                                                                                                       01-0CT-1989 (Rel. 12, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
ANGIOTENSIN-CONVERTING ENZYME, SOMMIC ISOPORM PRECURSOR (EC 3.4.15.1)
(ACE) (DIPEPTIDYL CARBOXYPEPTIDASE I) (KININASE II) (CD143 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM AN ALTERNATIVE START SITE.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M2 (ZINC METALLOPROTEASE).
-!- DATABASE: NAME-FROW; NOTE-CD guide CD143 entry;
WWW-"http://www.ncbi.nlm.nlh.gov/prow/cd/cd143.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 89071703.
Soubrier F., Alhenc-Gelas F., Hubert C., Allegrini J., John M.,
Tregear G., Corbol P.;
"Two putative active centers in human angiotensin I-converting enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               high-
amino
                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Purification of human lung angiotensin-converting enzyme by performance liquid chromatography; properties and N-terminal
641 NPEKNNLIQLNYRYANQEYIDQNLGKSANAYQQDIQQVGL--VVGWEIA 687
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-LUNG;
MEDLIKK; 90110025.
Takeuchi K., Shimizu T., Ohishi N., Seyama Y., Takaku F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     revealed by molecular cloning.";
Proc. Natl. Acad. Sci. U.S.A. 85:9386-9390(1988).
                                                                                                                                           PRT; 1306 AA.
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                                                                                                                                                                                                (Rel. 12, Created)
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                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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PIR; PQ0004; PQ0004.
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01-0CT-1989
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P12821;
                                                                              RESULT 13
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us-09-430-029-5.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SIDE---LRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFEDA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPEG-IDLVTDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNTTTFTSKTLLQKNMQIA 694
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                              SOMATIC
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                                                                                                                             SIMILARITY).
                                                                                                                                                (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches 214; Indels 321;
                                                                                                                                                                                                                                                                                                                                                                            Length 1306;
                              ANGIOTENSIN-CONVERTING ENZYME,
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-> R (IN REF. 2).
IB33BCA7301A26AA CRC64;
                                      ISOFORM.
EXTRACELLULAR (POTENTIAL).
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                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL)
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2 (BY SIMILARITY).
2 INC 2 (CATALYTIC) (
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18.8%; Pred. No. 7.3;
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Matches 142; Conservative
Alternative splicing.
SIGNAL 1 29
                                               677
695
714
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1191
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Best Local Similarity
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                                                                                                                                                                                          979 NLEDL/VVAHHEMGHIQYFMQYKDLPVALREGANP---GFHEAIGDVLALSVSTPKHLHSL 1035
                                                                                                                                                                                                                                                                      1036 NLLSSEGGSDEHDINFLMKMALDKIAFIPFSYLVDOWRWRVFDGSITKENYNQEWWSLRL 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE PEPN SUBFAMILY.
·HQAWSTFYG----FNAASAFHTWVPTED--EMGWLSAKY 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klein J.R., Klein U., Schad M., Plapp R.; "Cloning, DNA sequence analysis and partial characterization of pepN, a lysyl aminopeptidase from Lactobacillus delbruckii ssp. lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUT. J. Biochem. 217:105-114(1993).
--I- FUNCTION: AMINOPEDIASE WITH BROAD SUBSTRATE SPECIFICITY TO SEVERAL PEPTIDES. OPTIMUM ACTIVITY IS MEASURED AT PH 6.5-7.0 AND TEMPERATURES 54-55 DEGREES CELSIUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactobacillus delbrueckii (subsp. lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                921 FKEADDFFTSLGLLPVPPEF--WNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKQCTTV
                                      ----HINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDT---TEAMLKQGWTPRRM
                                                                                                                                                                                                                                NYLGNK-------PQKYVQAWLPVHQ
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SUBCELLULAR LOCATION: CYTOPLASMIC. IT MAY BE SECRETED THROUGH
AN UNKNOWN MECHANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
AMINOPEPTIDASE N (EC 3.4.11.2) (LYSYL AMINOPEPTIDASE) (LYS-AP)
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ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
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PRINTS; PR00756; ALADIPTASE.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Hydrolase; Metalloprotease; Aminopeptidase; Zinc.
                                                                                                                                                      394 ------MKTLPMLCQTCQIPMLFTEPGNPTKIGARES-
                                                                            368 PDSFDRYYR-----PRFDHWG----EOARAGNR----
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-!- SUBUNIT: MONOMER (BY SIMILARI
-!- SUBCELLULAR LOCATION: CYTOPLA
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291
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  328 EGKDHIS--
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P37896;
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ACT_SITE
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                                                                                                                                                                      AVIDAFTQNNAFLGVSD----ARYINALKL-FLQGVTPLEYLAHRGFAHVGRHFTGEGAR 130
                                                                                                                                                                                                                                 131 IACQMQ--SIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPK---SFFEDAY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 KEVPFTFGDDFEGIKIEAGKTGEAVIALDYSA---PLTDIWMGIYPSYYQVDGVKKELIG 115
                                                                                                                                                                                          116 TQFETTFAREAFPCVDEPEAKATFSLALKFDEHEGETVLANMPEDRVEN-GVHYFKETVR 174
                                                                                                                                                                                                                                                      SSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIEC 245
                                                                                                                                                                                                                                                                                                                                                            287
                                                                                                                                                                                                                                                                                                                                                                                     ----LLLDPDNTTLEMKKLVATVVTHELAHQWFGDLVTMEWWDNLWLNESFANMMEYLSV 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                    381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             382 VMVRSLLGDEALRKGLKRYFDKHKFG---NAAGDD--LWDALSTATDLNIGEIMHTWL-- 434
                                                                             Gaps
                                                                                                          -DWDKWVDPFRLTM----DAYWKYQGEKEKKLY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus suis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus suis type 2.";
Infect. Inmun. 60:2361-2367(1992).
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CELL WALL.
-!- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS
IN THE REGION OF THE MEMBRANE ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYOALRAEAGHALRIN-----VGNNSHFIVKYDQTIMDDIMKEAKDLDPVSQLQLLQDL
                                                                                                                                                                                                                                                                                                                                                        246 IKFLLEQDPDNVPIVQRWI------DKWF-----WRGYRLLTLVAMMDYMQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHLEPNWHIWEMFQTSEAAALTRDATDGVQSVHVEVNDPAEIDALFDGAIVYAKGSRML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDEMGW -- LSAKYPDSFDRYYRPRFDHWGEQARAGNRFYMK ----TLPMLCQTCQIPM -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LFTEPGNPTKIGARESNYLGNKFHF------CSDHCKDIFDHEPQKYVQAWLPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=SERGITYPE 2 / D282;
MEDLINE; 92267650.
Smith H.E., Vecht U., Gielkens A.L., Smits M.A.;
"Cloning and nucleotide sequence of the gene encoding the 136-kilodalton surface protein (muramidase-released protein) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
01-0CT-1994 (Rel. 30, Last annotation update)
MURAMIDASE-RELEASED PROTEIN PRECURSOR (136 KDA SURFACE PROTEIN)
                                                                             Indels 173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HQIHQG-NCFPPDADPGAEGFDPLAAVLDYYAVTMGRDNL-DF--DGSEDQKNFAA
                                              Length 842;
5C65781B08444D4F CRC64;
                                                                                                                                                                                                                                                                                                                          QT-PYPLPQSL-----QLALPDFSAGAMENWGLVTYREAY-
                                             Score 92.5; DB 1;
Pred. No. 6;
.; Mismatches 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1256 AA
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                                                                             71;
95216 MW;
                                              3.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                  KRVMSWRESWEMYAEQNGG-
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                          KVFPY --- DRYEGIKIH-
 AA;
                                                           Similarity
842
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                                                          Local Simily
hes 115;
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SEQUENCE
                                              Query Match
                                                                             Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                    CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    397 YDYVATITKAVQGPYPKG-----TVYLAGTVQKD-----TVQYKVIREIVENDQAVL 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 FEYVLTNLLFV--PFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIECIKFLLEQDPDNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            444 KFYYLDPTYKGEVD---WRGTDTTGFIBLLTTSPTTYKVGTIYDYNINSKITAPFTIDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        288 KRVMSWRESWEMYAEQN-GGALFKDLARY-GIREPKGWQDACEGKDHISHQAWSTFYGFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNVMVFKES-----EQNEQGSKYRVIAQWSGDETTKG----IYGKIYIATQVWTTKLGTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  406 IPMLFTEPG-----NPTKIGARESNYLGNKFHFCSDHCKDIFDHEPQKYVQAWLPVHQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----FWPAGVQNTLRNATPATAVETTYIYKESSKYGDVIVEYYDTDGKQIVNSVYDTPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 AASAFHTWVPTEDEMGWLSAKYPDSFDRYYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                        Length 1256;
                                                                                                                                                                                               MURAMIDASE-RELEASED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                              135795 MW; DCF7F65242F14341 CRC64;
                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL). MEMBRANE ANCHOR.
                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PIVQRWIDKWFWRG-----YRLLTL-----VAMMMDY-
                                                                                                                                                                                                                                                                                                                                                                                                                               92;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 90.5; I
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                    PIR; A48829; A43829.

PPAM; PP00746; Gram_pos_anchor; 1.

PROSITE; PS00343; GRAM_POS_ANCHORING; 1.

Repeat; Transmembrane; Cell wall; Signal.
                                                                                                                                                                                                                                                                                                                                                  PROTEINS
                                                                                                                                                                                                                                                                             LARGE.
                                                                                                                                                                                                                                                                                             SMALL
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                                                                                                             EMBL; X64450; CAA45781.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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1231
1248
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681
861
1006
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1195
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Best Local Similarity
Matches 70; Conserv
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TRANSMEM
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Search completed: September 26, 2000, 20:30:09

Job time: 433 sec

101

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

- protein search, using sw model OM protein ; Search time 82.1 Seconds
(without alignments)
388.947 Million cell updates/sec September 26, 2000, 20:24:16 Run on:

US-09-430-029-5 Title:

Perfect score:

1 MDTPTLKKKLGLKDRYAAMT......FDGSEDQKNFAAWRGQATRN 516 Sednence:

Scoring table:

178050 seqs, 61884766 residues Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

178050 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

Database :

PIR\_64:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

		æ			SUMMARIES	
Result No.	Score	Query Match	Length	DB	QI	Description
П	1854.5		516	-	S44306	phenol 2-monooxyge
71	1846.5	64.3	517	Н	D37831	
ĸ	1795		511	-	S47290	
4	254.5	6.8	527	7	JQ0702	Φ
2	211	•	525	7	S15207	methane monooxygen
9	115	•	852	~	GNLJGA	pol polyprotein -
7	111.5	3.9	852	a	S29358	pol protein - bovi
80	107.5	3.7	852	J	GNLJGB	
Q	104	3.6	549	Н	A24436	alpha-amylase (EC
10	103	3,6	526	(7	T01089	hypothetical prote
11	0	3,6	550	7	B69022	methyl coenzyme M
12	99.5	3.5	1032	~	S74487	hypothetical prote
13	66	3.4			E28544	methyl coenzyme M
14	S.	3.4	785	~	H72228	hypothetical prote
15	96.5	3.4	1209	7	T31657	reverse transcript
16	95	٠	782	Η	G64157	probable organic s
17	95	3.3	1336	r	T17479	hypothetical prote
18	S	3.3	1455	Н	A48925	mannose receptor p
19	94.5	3.3	1306	~	A31759	peptidyl-dipeptida
20	94	3.3	395	7	T45547	arylsulfatase acti
21	94	3.3	452	~	T28094	hypothetical prote
22	93.5	3,3	333	Н	S47288	phenol 2-monooxyge
23	93.5		579	7	JW0071	asparagine synthas
24	92.5	•	843	7	S38364	membrane alanyl am
25	91.5	•	548		ALBSF	alpha-amylase (EC
26	90.5		362	7	H69785	-
27	90.5	3.2	1256	Н	A43829	muramidase-release
28	06		549	급	<b>4</b> 5	alpha-amylase (EC
29	89.5	3.1	1258	7	JC5765	inositol polyphosp

hypothetical prote	probable regulator	phenol 2-monooxyge	methionyl-tRNA syn	1-phosphatidylinos	hypothetical prote	alpha-amylase (EC	asparagine synthas	lysine decarboxyla	alpha-amylase (EC	arylphorin alpha c	CrylAc toxin-bindi	probable cell wall	alpha-qlucan synth	probable cell wall	protein 9377 - Pla
T23844	A35159	A45730	B75074	A36369	T16430	A54541	AJPMN2	B64743	573087	A34434	T18533	T41740	T43435	T43731	T18414
C) (	?	C)	~	a	C1	Н	Н	7	C3	N	7	m	7	~	7
245	405	671	722	875	848	549	583	713	261	702	1009	1210	2410	2410	3119
3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.0	3.0	3.0	3.0	3.0	3.0	3.0
6 8	90	68	68	68	88.5	88	88	88	87.5	87.5	87.5	87.5	87.5	87.5	87.5

# ALIGNMENTS

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	z
RESULT 1 S44306	phenol 2-monooxygenase (EC 1.14.13.7) component N N; Alternate names: phenolhydroxylase chain D

Pseudomonas putida

C.Species: Pseudomonas putida
C.Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999
C.Scossion: E58972: S54765; S44306; S47417
Gene 151, 29-36, 1994
A.Fitle: Cloning and sequences of the first eight genes of the chromosomally encoded A.Reference number: AS8972; MUID:95129877
A.Scossion: E58972
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1516 cNGA
A.Residues: 1516 cNGA
A.Residues: Localization P35X (NCB1 9869)
A.Note: the nuclectide sequence was submitted to the EMBL Data Library, April 1994
R.Hermann, H.; Mueller, C.; Schmidt, I.; Mahnke, J.; Petruschka, L.; Hahnke, K.
MOI. Gen. Genet. 247, 240-246, 1995
A.Sterimental source: strain and organization of phenol degradation genes of Pseudomonas put A.Reference number: S54761; MUID:95272534
A.Status: preliminary; nucleic acid sequence not shown: translation not shown A.Status: preliminary; nucleic acid sequence not shown: translation not shown A.Status: preliminary; nucleic acid sequence not shown: translation not shown A.Status: preliminary such as submitted to the EMBL Data Library, July 1994
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
A.Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
A.Steperimental source: Strain H
A.Note: the nucleotide sequence component N
C.Scheetids: Oxidoreductase

Gaps 64.5%; Score 1854.5; DB 1; Length 516; ilarity 64.8%; Pred. No. 1.1e-142; Conservative 65; Mismatches 105; Indels 9; Query Match Best Local Similarity Matches 329; Conserva

ij

5 TLKKKLGLKDRYAAMTRGLGWETTYQPMDKVFPYDRYEGIKIHDWDKWVDPFRLTMDAYW 64 δ

qq

65 KYQGEKEKKLYAVIDAFIQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGRHF 124 OYq

184 δ

QΥ

Q

YSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMILGIE 244 185

Db 366 YPDTFDKYXRRFEFWREQQAKGERFYNDTLPHLCQVCQLPVIFTEPDDPTKLSLKSLVH 425  Qy 427 LGNKFHFCSDHCKDIFDHEPOKYVQAMLPVHQIHQGNCFPFDADPGAEGFDPLAAVLDYY 486    ::	RESULT 3 84720 phenol 2-monooxygenase (EC 1.14.13.7) chain mopN - Acinetob N.Alternate names: phenol hydroxylase C.Species: Acinetobacter calcoaceticus C.Date: 10.Sep-1999 #sequence_revision 10-Sep-1999 #text_ch C.Accession: S70083; 84730 R.Ehrt, S.; Schirmer, F.; Hillen, W. Mol. Microbiol. 18, 13-20, 1995 A.Fitle: Genetic organization, nucleotide sequence and regu A.Reference number: S70080; MIDE:96154937	600)	Ouery Match 62.5%; Score 1795; DB 1; Length 511; Best Local Similarity 64.1%; Pred. No. 7.1e-138; Matches 325; Conservative 60; Mismatches 112; Indels 10; Gaps 2; Qy 8 KKLGLKDRYAAMTRGLGWETTYQPMDKVFPYDRYEGIKIHDWDKWVDFFRLTMDAYWKYQ 67	QY         68 GEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGRHFTGE 127           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	126 QY 188 GPFEFLTAVSFSFEYVLTNILFVPFMSGAAYNCDMSTYTFGFSAQSDESRHWTLGIECIK 247	186   QY   248 FLLEQDPDNVPIVQRWIDKWFWRGYRLLTLVAMMMDYMQPKRVMSWRESWEMYAEQNGGA   307	306 QY 368 PDSFDRYYRPREDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTE-PGNPTKIGARESNY 426 11:11:11 11 1::	346   QY   427   LGNKFHFCSDHCKDIFDHEPQKYVQAWLPVHQIHQGNCFPPDADPGAEGFDPLAAVLDY 486	426 Qy 487 AVTMGRDNLDFDGSEDQKNFAAWRGQA 513
::	AKYPDSFDRYYRPREDHWGEOARAGNREYMKTLPMLCGTCOIPMLFTEPGNPTKIGARES	onas sp. ( _change 10 alysis of	A; Accession: D3 03.1 A; Status: preliminary A; Wolecule type: DNA A; Residues: 1-517 < NOR> A; Residues: 1-517 < NOR> C; Superfamily: phenol 2-monooxygenase component N C; Keywords: oxidoreductase	tch 64.3%; score 1846.5; DB 1; Length 517; sal Similarity 64.8%; Pred. No. 4.8e-142; 328; Conservative 63; Mismatches 106; Indels 9; Gaps KKKLGIKDRYAAAMTRGLGWETTYQPMDKVFPYDRYEGIKIHDWDKWVDPFRLTMDAYWKY 66	QGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGRHFTG	EGARIACOMOSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFEDAYS	KFLLEQDPDNVPIVQRWIDKWFWRGYRLLTLVAMMMDYMQPKRVMSWRESWEMYAEQNGG   :	ALFKDLARYGIREPKGWODACEGKDHISHQAWSTFYGFNAASAFHTWVFTEDEMGWLSAK 	YPDSFDRYYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKIGARESNY 426

fr

```
Poll polyprotein - bovine leukemia virus (strain Australia)

N; Contains: endonuclease (EC 3.1.-.-); RNA-directed DNA polymerase (EC 2.7.7.49)
C; Species: bovine leukemia virus, BLV
A; Note: host Bos sp. (cattle)
C; Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 16-Jul-1999
R; Coulston, J; Naif, H; Brandon, R; Kumar, S.; Khan, S.; Daniel, R.C.W.; Lavin, M. J. Gen. Virol. 71, 1737-1746, 1990
A; Title: Molecular cloning and sequencing of an Australian isolate of proviral bovine A; Reference number: JQ0554, MUID:90362060
A; Accession: JQ0555
A; Accession: JQ0555
A; Accession: JQ0554, MUID:90362060
A; Accession: JQ0555
A; Accession: JQ0555
A; Accession: JQ0554
A; Residues: DNA
A; Residues: DNA
A; Residues: DNA
A; Residues: DBB:DD0647; NID:9221051; PIDN:BAA00544.1; PID:d1000999; PID:9221
A; Note: this reading frame extends between two stop codons and does not begin with a A; Note: the authors translated the codon CCC for residue 514 as Gln
C; Comment: The precise boundary between RNA-directed DNA polymerase and endonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: pol
C,Superfamily: pol polyprotein
C,Keywords: endonuclease; hydrolase; nucleotidyltransferase; polyprotein; reverse tra
R;Fox, B.G.; Liu, Y.; Dege, J.E.; Lipscomb, J.D.
J. Biol. Chem. 266, 540-550, 1991
A;Title: Complex formation between the protein components of methane monooxygenase : A;Reference number: A39049; MUID:91093180
A;Reference number: A39049; MUID:91093180
A;Reference preliminary
A;Residues: preliminary
A;Residues: 2-16 <FOx>
C;Genetics: mmoX
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | :: : |:: | : : | :: | 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 FLGVSDARYINALKLFLQGVTPLE----YLAHRGFAHVGRHFTGEGARIACQMQSIDELR 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            143 HYQTETHAMSIYNKFFNGFHHS------NQWFDRVWYLSVPKSFFEDAY-SSGPFEF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260 DPASAKFLNTDLNNAFWTQQKYFTPVLGYLFEYGSKFKVEPWVKTWNRWVSEDWGGIWIG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147 H----THQCAFINHYYSKHYHDPAGHNDARRTRAIGPLW--KGMKRVFADGFISRDAVEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201 SVNLQLVGDTCFTNPLIVAVTEWAIGNGDEITPTVFLSVETDELRHMANGYQTV-VSIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 DPDNVPIVQRWIDKWFWRGYRLLT-LVAMMMDYMQPKRVMSWRESWEMYAEQN-GGALFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 RLGKYGV-ESRVLRDAKRDAYWAHHDL-----ALAAYAMWPLAFARLALPDEEDQAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      193 LTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGTECIKFLLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 LSAKYPDSFDRYYRPRFDHWG----EQARAGNRFYMKTLP----MLCOTCOIPMLFTEP
                                                                                                                                                                                                                                                                                                                                                                                                              94;
                                                                                                                                                                                                                                                                                                                                                         Length 525;
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                                                                                                                                                                                                                                                                                                                                                                                                              196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 KIHDWDKWVDPFRLTMDAYWKYQGEKEKKLY-AVIDAFTQNNA
                                                                                                                                                                                                                                                                                                                                                      7.3%; Score 211; DB 2;
21.0%; Pred. No. 2.1e-09;
Live 71; Mismatches 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        414 GNPTKIGA-RESNYLGNKFHFCSDHCKDIFDHEPQKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SLAKGTGSLRVHEFNGKKHSLTDDWGERQWLIEPERY
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                                                                                                                                methane monooxygenase (EC 1.14.13.25) component A alpha chain - Methylococcus capsulatus
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Mol. Microbiol. 5, 335-342, 1991
A/Title: Molecular analysis of the methane monooxygenase (MMO) gene cluster of Methylosi A; Reference number: $15207; MUID:91251762
A; Accession: $12207
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trichospor
                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-527 <STA>
C;Comment: This multicomponent enzyme catalyzes the conversion of methane to methanol
                                                                                                                                                                                                                                                                                               cluster of Methylococcus capsulatus (Bath).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               methane monooxygenase (EC 1.14.13.25) component A alpha chain - Methylosinus C;Species: Methylosinus trichosporium C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Jun-1999 C;Accession: S15207; A30049
                                                                                                                                                            C;Species: Methylococcus capsulatus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --SNFLEVGEYNAIAATGMLWDSAQAAEQKNGYLAQVLDEIRH----THQCAYVNYYFAK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 AHRGFAHVGRH----FTG---EGARIACQ-----MOSIDELRHYQTETHAMSTYNKFF-- 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NG---FHHSNQWFDR----VWYLSVPKSFFEDAYSSGPFEFLTAVSFSF------EYVLT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIECIKFLLEQDPDNVPIVQRWID 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KWFWRGYRLLT-LVAMMMDYMQPKRVMSWRESWEMYA-EQNGGALFKDLARYGIREPKGW 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   273 NAFWIQOKYFTPVLGMLFEYGSKFKVEPWVKTWNRWYYEDWGGIWIGRLGKYGVESPRSL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWLSAKYPDSFDRYYRPRFDHWG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KDAKQDAYWAHHDLYLLAYALWPTGFFRLALPDQEEMEWFEANYPGWYD-HYGKIYEEW- 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 DPFRLTMDAYWKYQGEKEKKLYAVID-AFTQNNAFLGVSDARYINALKLFLQGVTPLEYL 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -RARG------CEDPSSGFIPLMWFIENNHPIYIDRVSQVPFCPSLAKGAS 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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A;Cross-references: EMBL:X55394; NID:g44613; PIDN:CAA39068.1; PID:g44614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 NGQDPAGHNDARRTRTIGPLW--KGMKRVFSDGFISG-----DAVECSLNLOLVGEACFT
                                                                                                                                                                                                                                            V.; Salmond, G.P.C.; Dalton, H.; Murrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |:| EQFKLIAKEYARMEAVKDERQFGSLQVALTRLNAGVRV-HPKWNETMKVV--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 254.5; DB 2
Pred. No. 6.1e-13;
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                                                                                                                                                                                                                                    Ristainthorpe, A.C.; Lees, V.; Salmond, G. Gene 91, 27-34, 1990
A; Fitle: The methane monooxygenase gene cl
A; Reference number: JQ0700; MUID:90382694
A; Accession: JQ0702
510
484 NFNVGADNLDIEGSPDQQRWKKWKGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65;
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Best Local Similarity 24.25
Matches 109; Conservative
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C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                           Accession: JQ0702
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36;													e and
sde	47	96 281	144	169 392	218	267	294	333	380	431	470		ay-1999 sequence
4.0%; Score 115; DB 1; Length 852; 18.7%; Pred. No. 0.23; .ive 81; Mismatches 252; Indels 248; Gaps	TYQPMDKVFPYDRYEGIKIH	VDPFRLTMDAYMKYQGEKEKKLYAVIDAFTQNNAFLGVSDARXI 9	FAHVGRHFTGEGARIAC-OMOSIDELRHY III	QTNQWFD1 	RVWYLSVPKSFFEDAYSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAY 2 ::	NGDMSTVTFGFSAQSDESRHMTLGIECIKFLLEQDPDNVPIVQFWID-KW 2	LYKSLLRHPAIFVGHVRSHSSASHPIASLNNY	ESWEMYAEQNGGALFKDLARYGIREPKGWQDACEGKDHI 3 VDQLLPLETPEQWHKLTHCNSRALSRWPNPRISAWDPRSPATLCETCQRLNPTGGGKMRT 6	SHQAWSTEYGFNAAS-AFHTWVPTEDEMGWLSAKYPDSFDKYYRPRFD 3 :	HWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKIGARESNYLGNKF 4	HECSDHCKDJFDHEPQKYVQAWLPVHQIHQGNCFPPDAD 4	PGAEGFDPLAAVLDYYAVIMGRDNLDFDGSEDQKN 505 	irus s, BLV evision 13-Jan-1995 #text_change 07-M urny, A.; Gilden, R.V. of bovine leukemia virus: nucleotide D:86045859
atch cal Similarity 134; Conservat		DWDKW	NALKLF		RVW ::  Ellqlw	NG       RGAYCLWKDH	FWRGYRLLTLVAMMMDYMQPKRVMSWR- :						RESULT 7  \$29958  pol protein - bovine leukemia v C;Species; bovine leukemia viru C;Date: 13-Jan-1995 #sequence_r C;Accession: \$2936  R;Rice, N.R.; Stephens, R.M.; B V;rology 142, 357-377, 1965  A;Ritle: The gag and pol genes A;Reference number: \$29356; MUIA A;Accession: \$23958  A;Status: preliminary A;Molecule type: DNA A;Residues: 1-852 <ric> A;Cross-references: EMBL:MU0987 C;Superfamily: pol polyprotein</ric>
Query M Best Lo Matches	Qy 3 Db 169	Qy 48 Db 229	Qy 97 Db 282	Qy 145 Db 333	Qy 170 Db 393	Qy 219 Db 446	Qy 268 Db 497	Qy 295 Db 553	Qy 334 Db 613	Qy 381 Db 673	Qy 432 Db 733	Qy 471 Db 793	RESULT 7 S29358 pol protein C.Species: 13 C.Date: 13- C.Accession R.Rice, N.R N.Trology 14 A.Title: The A.Referenc

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A;Note: the authors translated the codon TTC for residue 104 as Ser and CIA for resid C;Comment: Specific enzymatic cleavages may yield mature proteins including reverse t C;Genetics:
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C;Superfamily: pol polyprotein
C;Keywords: endonuclease; hydrolase; nucleotidyltransferase; polyprotein; reverse tra
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N; Contains: endonuclease (EC 3.1.-.-); RNA-directed DNA polymerase (EC 2.7.7.49)
C; Species: bovine leukemia virus, BLV
A; Note: host Bos sp. (cattle)
C; Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 01-May-1998
C; Accession: A03960
R; Sagata, N; Yasunaga, T; Tsuzuku-Kawamura, J; Ohishi, K.; Ogawa, Y; Ikawa, Y.
Proc. Natl. Acad. Sci. U.S.A. 82, 677-681, 1985
A; Title: Complete nucleotide sequence of the genome of bovine leukemia virus: its e A; Reference number: A94063; MUID:85140159
A; Mccession: A03960
A; Molecule type: DNA
                                                       30;
                                                                                                                                    :|| :::
169 SPTEEQRSQCYQALAARLRDLGFQVASEKTRQTPSPVPFLGQMVHNQIVTYQSLPTLQIS 228
                                                                                                                                                                                                                                                                                                                                                                                                                                            333 QIPLIDNQASPWGLILLIGCQYLQTQALSSYAKPILKYYHNLPKITSLDNWIQSSEDPRVQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              393 ELLQLW----PQISSQGIQPPGPWKTLITRAEVFLTP-QFSPEPIPAALCL--FSDGATG 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 VDQLLPLETPEQWHKLTHCNSRALSRWPNPRISAWDPRSPATLCETCQRLNPTGGGKMRT 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97 NALKLFLOGVTPL-EYLAHRG-----FAHVGRHFTGEGARIAC-QMQSIDELRHY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 SHQAWS-----TFYGFNAAS-AFHTWVPTEDEMGWLSAKYPDSFDRYYRPRFD--- 380
                                                          Gaps
                                                                                                                                                                                                         48 DWDKWVDPFRLTM-----DAYWKYQGEKEKK----LYAVIDAFTQNNAFLGVSDARYI 96
                                                                                                       3 TPTLKKKLGLKDRYAAMTRGLGWET-----TYQPM-----DKVFPYDRYEGIKIH 47
                                                                                                                                                                                                                                                                                                                                               -----LQGIAELRQALSHNARSRYNEQEPILLAYV--HLTRAGSTLVLFQKGAQFPLAYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               497 LYSLLRTLVLGA----WLQPDPVPSYALLYKSLLRHPAIFVGHVRSHSSASHPIASLNNY
                                                                                                                                                                                                                                              ----SPISLHQLQAVLGDLQWVSRGTPTTRRPLQLLYSSLKGIDDPRAIIQLSPEQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ESWEMYAEQNGGALFK----DLARYGIREPKGWQDACE-----GKDHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ETHAMSTYNKFFNGFHHS-----NQWFD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 ---RVWYLSVPKSFFEDAYSSGPFE-----FLTAVSFSFEYVLTNLLFVPFMSGAAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 NG------DMSTVTFGFSAQSDESRHMTLGIECIKFLLEQDPDNVPIVQRWID-KW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                381 HWGEQAR----AGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKIGARES----NYLGNKF
                                                    214; Indels 207;
     Length 852;
3.9%; Score 111.5; DB 2;
19.0%; Pred. No. 0.45;
tive 70; Mismatches 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268 FWRGYRLLTLVAMMMDYMQPKRVMSWR--------
                                                  Matches 115; Conservative
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-852 <SAG>
                                                                                                                                                                                                                                                                                                                                                                                                            145 QT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 733 HLDEPH 738
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type; alpha-amylase core homology heat-stable protein; hydrolase; polys
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                 in multiple copies
                                                                                                  A.Genome: plasmid
A.Start codon: GTG
A.Start codon: GTG
C.Function:
A.Pathway: glycogen/starch degradation
A.Pathway: glycogen/starch degradation
C.Superfamily: alpha-amylase, amyloliquefaciens type; alpha-amylase core homology
C.Superfamily: alpha-amylase wayloliquefaciens type; alpha-amylase core homology
C.Reywords: extracellular protein; glycosidase; heat stable protein; hydrolase; F.13-449/product: alpha-amylase factaus sexperimental cMAT>
F.35-549/product: alpha-amylase core homology cAMX>
F.35-549/product: alpha-amylase core homology cAMX>
F.35-549/product anylase core homology cAMX>
F.35-549/product appla-amylase core homology cAMX>
F.35-549/product appla-amylase core homology cAMX>
F.35-549/product appla-amylase sore homology cAMX>
F.368,298,365/Active site: asp, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: T0PP11.12 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 14-May-1999
C;Accession: T01089 #sequence_revision 12-Feb-1999 #text_change 14-May-1999
C;Accession: T01089
R;Kaplan, N.; Johnson, D.; Schutz, K.; Gnoj, L.; Hoffman, J.; Till, S.; de la Bai submitted to the EMBL Data Library, November 1998
A;Description: Sequence of A. thaliana BAC T10Pl11 from chromosome IV.
A;Accession: T01089
A;Accession: T01089
A;Accession: T01089
A;Accession: T01089
A;Accession: T01089
A;Residues: 1-526 <AAP>
A;Cross-references: EMBL;AC002330; NID:92262135; PID:93892049
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----SFFPDWLSDVRSQTGKPLFTVG----EYWSY---- 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 RHFTGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---AVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGYPCVFYGDYYGIPQYNIPS 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 LKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMY 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 EDAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 WKYQGEKEKKLYAVIDAFTQNNAFL--GVSDARYINALKLFLQGVTPLEYLAHRGFAHVG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----VDPFRLTMDAY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 YAEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVP---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 RGIGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKSWGKWYVNTTNIDGFRLDAVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 549;
C:Comment: Alpha-amylase genes have been found on plasmids and C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 TASKSGGTFDMRT-----LMTNTLM------KDQPTL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------WRGYRLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 -----DINKLHNYIMKIN--GTMSLFDAPLHN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.6%; Score 104; DB 1; L. Best Local Similarity 18.3%; Pred. No. 1; Matches 82; Conservative 43; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - KIHDWDKW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276 ----TLVA-----MMMDYMQPKRVMSW-RE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDEMGWLSAKYP--DSFDRYYRPRFDHW 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 GIECIKFLLEQDPDNVPIVQRWIDKWF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 RGLG--WETTYQPMDKVFPYDRYEGI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273 IKF--
                                                                             A; Gene: amys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pAT5
                                          30;
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C; Jaces State: 05-Jun-1987 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C; Accession: A24436; 13977 #sequence_revision 18-Aug-1995 #text_change 18-Jun-1999
C; Accession: A24436; 13974 #sequence number: A24436; MUID:85234394
A; Reference number: A24436; MUID:85234394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alpha-amylase (EC 3.2.1.1) precursor - Bacillus stearothermophilus plasmid N.Alternate names: 1,4-alpha-D-glucan glucanohydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333
                                                                                                                                                                                                                                                                                                                                                                                                                       446 RGAYCLWKDHLLDFQAVPAPESAQKGELAGLLAG-----LAAAPPEPVNI---WVDSKY 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 QTPLITDNQASPWGLLLLLGCQYLQTQALSSYAKPILKYYHNLPKISLDNWIQSSEDPRVQ 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 ---RVWYLSVPKSFFEDAYSSGPFE-----FLTAVSFSFEYVLTNLLFVPFMSGAAY 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- DMSTVTFGFSAQSDESRHMTLGIECIKFLLEQDPDNVPIVQRWID-KW 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    294
                                          Gaps
                                                                                                         -DKVFPYDRYEGIKIH 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A;Residues: 1-45 <RES>
A;Cross-references: GB:M62638; NID:g142514; PIDN:AAA22242.1; PID:g142515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::| |:: | |:: | |:: | |:: | |:: | |:: | |:: | |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ESWEMYAEQNGGALFK----DLARYGIREPKGWQDACE-----GKDHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         613 IORGWAPNHIWQADITHYKYKQFIYALHVFVDTYSGATHASAKRGLTTQTTIEGLLEAIV
                                                                                                                                                                                                                                        DWDKWVDPFRLTM-----DAYWKYQGEKEKK-----LYAVIDAFTQNNAFLGVSDARYI
                                                                                                                                                                                                                                                                                                              ----SPISLHQLQAVLGDLQWVSRGTPTTRRPLQLLYSSLKRHHDPRAIIQLSPEQ--
                                                                                                                                                                                                                                                                                                                                                                             NALKLFLQGVTPL-EYLAHRG-----FAHVGRHFTGEGARIAC-QMQSIDELRHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            497 LYSLLRTLVLGA----WLQPDPVPSYALLYKSLLRHPAIVVGHVRSHSSASHPIASLNNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----TFYGFNAAS-AFHTWVPTEDEMGWLSAKYPDSFDRYYRPRFD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HWGEQAR----AGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKIGARES----NYLGNKF
                                          207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ETHAMSTYNKFFNGFHHS-----NOWFD---
                                      214; Indels
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A.Experimental source: plasmid pAT5
A.Note: amino end of the mature protein also determined
E.Jorgensen, P.L.; Hansen, C.K.; Poulsen, G.B.; Diderichsen,
Gene 96, 37-41, 1990
A:Title: In vivo genetic engineering: homologous recombinatic
                                                                                                     TPTLKKKLGLKDRYAAMTRGLGWET-----TYQPM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
       0.94;
                                      Mismatches
          Š.
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A; Accession: 139777
       Pred,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FWRGYRLLTLVAMMMDYMOPKRVMSWR
                                          70;
       19.0%;
                                          Conservative
   Best Local Similarity
Matches 115; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-549 <NAK>
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F;481/Binding site: coenzyme B (Asn) #status predicted
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A; Residues: 1-1032 <KAN>
                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                   85;
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Matches 5
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                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Methylozonczyme M reductase (EC 1.8.-.-) I alpha chain - Methanobacterium thermoautotrop (Species: Methanobacterium thermoautotrophicum A, Variety: strain Delta H
C.Date: O's-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 11-Jun-1999
C.Accession: B69022; $78579
C.Accession: B69022
C.Accession: C.Acce
A;Introns: 61/1; 145/3; 184/3; 205/1; 237/3; 262/3; 309/1; 322/3; 392/3; 415/2; 435/3
A;Note: T10P11.12
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C; Superfamily: methyl coenzyme M reductase alpha chain
C; Superfamily: methyl coenzyme M reductase sets is nickel; oxidoreductase
C; Seywords: heterobexamer; metalloprotein; methanogenesis; nickel; oxidoreductase
F; 2-550/Product: methyl coenzyme M reductase I alpha chain #status experimental <M
F; 247/Binding site: coenzyme F430 nickel
F; 333/Active site: Tyr #status predicted
F; 444/Binding site: coenzyme M (Tyr) #status predicted
                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                                                                                                                                          294
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -NGFHHSNQWFDRVWYLSVPKSFFEDAYSSGPFEFLTAVSFSFEYVLT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         206 NILFVPFMSGAAYNGDM----STVTFGFSAQSDESRHMTLGIECIKFLLEQDPDNVPIVQ 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 QLAHEVAEKHVAIEGDLVVKPSDEHFWFSKPQ-----IVLYLIHFILFQNAFEIAFF- 388
                                                                                                                                                                                                                                                                                          237
                                                                                                                                                                                                                                                                                                                                                  -NALKLFLQGVTPLEYLAHR-GFAHVGRHFTGEGARIACQMQSIDELRHYQTETHAMSTY 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----FWIWVTYGFDSCIMGQVRYIVPRLVIGVFIQVLCSYSTLPLYAIVSQMGSSFKKAI 444
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                  45 KIHDWDKWVDPFRLTMDAYWKYQGE----REKKLYAVIDAFTQNNAFLGVSDARYI---- 96
                                                                                                                                                                                                                                                                                                                                                                                  184 RIHOWKKWEDSI-----ADEKFDPETALRKRRVTHVHNHAFIKEH-FLGIGKDSVILGWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---TYFWIAFI--PFALLLAVGTKLEHVIA
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                                                                                                                                                                          43; Mismatches 130; Indels
                                                                                                                        Length
                                                                                                                     DB 2;
                                                                                                                  Score 103; DB Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RWIDKWFWRGYRLLTLVAMMMDYMQPK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 FKDLARYGIREPKGWQDACEGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           445 FEENVOVGL --- VGWAQKVKQK 463
                                                                                                               3.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 LWIFVVIFLLLNVNGWH----
                                                                                                                                                                          71; Conservative
                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                            155 NKFF--
                                                                                                                  Query Match
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Species: Synechocystis sp.
A;Variety: PCC 6803
C;Accession: S74487
B;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, A.; Kixaneko, T.; Sato, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys S.
A;Reference number: S74322; MUID:97061201
A;Accession: S74487
A;Status: nucleic acid sequence not shown; translation not shown
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                                                                17;
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                                                                                                                          141 LRHYQTETH----AMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFED------AYSSGPF 190
                                                                                                                                                                                    146 VQEHMVETHPALVADSYVKVFTGNDEIADEIDPAFVIDINKQFPEDQAETLKAEVGDGIW 205
                                                                                                                                                                                                                                                                                        206 QVVRIPTIVSRTCDGATTSRWSAMQIGMSMISAYKQAAGEAATGDFAYAAKHAEVIHMGT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RYGIREPKGWQDACEGK 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --WLSAKYPDSFDR 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                484
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                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54 DPFRLIMDAYWKYQGEKEKKLYAVIDAFTQNNAF----LGVSDA-----RYI-NALKL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 EFL---TAVSFSFEYVLT---NLLFVPFMSGAAYN---GDMSTVTFGFSAQSDESRHMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   427 WYLSMYLHKEQHSRLG--FYGYDLQDQCGASNVFSIRGDEGLPLELRGPNYPNYAMNVGH
                                                                                                                                                                                                                                                                                                                                                                                                                                      -GYLADICQSSRVNYEDPVRVSLDVVATGAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  374 YYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKI-GARESNYLGNKFH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FCSDHCKDIFDHEPQKYVQAWLPVHQIHQGNCFPPDADPGAEGFDPLAAVLDYYAVIMGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---PHAARGDAFVFNPLV----KIAFAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --LDVASEVTFYGLEQYEEYPALL--EDQFGGSQRAAVVAAAAGCSTAFATANAQTGLSG
                                                                Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. (strain PCC 6803)
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   Length 550;
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                                                                                                                                                                                                                                                                                                                                                                         242 GIECIKFLLEQDPDNVPIVQRWIDKWFWRGYRLLTLVAMMMDYMQPKRV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.5%; Score 99.5; DB 2; 20.5%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100;
   ;
;
3.6%; Score 103; DB
llarity 19.5%; Pred. No. 1.3;
Conservative 54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 DHISHQAWSTFYGFNAASAFHTWVPTEDEMG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 WRESWEMYAEQNGGALFKDLA-
                                                                                                                                                                                                                                                                                                                                                                                                                                   266 YLPVRRARGENEPGGVPF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S74487
hypothetical protein sll1060 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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516 DNLVFDFTNVRGEFA 530
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	OY 379 FDHWGEQARAGNRFYMKILPMLCQTCQIPMLFTEPGNPTKI-GARESNYLGNKFHFCSDH 437  :   :             : :              bb 432 YLHKEQHSRLGFYGYDLQDQCGASNVFSIRGDEGLPLELRGPNYPNYAMNVGH 484  OY 438 CKDIFDHEPQKYVQAWLPVHQIHQGNCFPPDADPGAEGEDPLAAVLDYYAVTMGRDNLDF 497    Db 485QGEYAGISQA	RESULT 14 H7228 hypothetical protein TM1624 - Thermotoga maritima (strain MSB8) C; Species: Thermotoga maritima C; Species: Thermotoga maritima C; Date: Il-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999 C; Accession: H7228 C; Accession: H7228 R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, C.M. Nature: Byidence for lateral gene transfer between Archaea and Bacteria from genome A; Reference number: A72200; MUID:99287316 A; Status: preliminary A; Status: preliminary A; Status: DNA A; Cross-references: GB:AE001806; GB:AE000512; NID:94982196; PID:94982197; TIGR:TM1624 C; Genetics: C; Genetic		OY 127 EGALIACQ
Db 768 LVDAXNGDVRFFTIDKQDPLINAWQKIFPELFLPFSSMPSTLKSHIRYPVDMFSTQSERL 827  Qy 148 -THAMSTVNKFFNGFHHSNQWFDKVWYLSVPKSFFEDAYSS-GPFEFLTAVSFSFEY 202	RESULT 13 E2854 methyl coenzyme M reductase (EC 1.8) I alpha chain - Methanobacterium thermoautotrop (5.5pecies: Methanobacterium thermoautotrophicum A; Variety: Strain Marburg (5.5pecies: Methanobacterium thermoautotrophicum A; Variety: Strain Marburg (5.5pecies: Methanobacterium thermoautotrophicum A; Variety: Step-1999 #sequence_revision 10-Sep-1999 #text_change 15-Oct-1999 (5.Accession: E28544; S78576 R; Bokranz, M.; Baeumner, G.; Allmansberger, R.; Ankel-Fuchs, D.; Klein, A. J. Bacteriol. 170, 568-577, 1988 A; Fitle: Cloning and characterization of the methyl coenzyme M reductase genes from MethA; Reference number: A91891; MUID:88115150	D:g44612 bacterium cof biolog gumaed 3 gumaed 3	de and methane A: Pathway: methanogenesis A: Pathway: methanogenesis C: Superfamily: methyl coenzyme M reductase alpha chain C: Superfamily: methyl coenzyme M reductase alpha chain *status experimental C: Superfamily: methyl coenzyme M reductase I alpha chain *status experimental F: 2-550/Product: methyl coenzyme F430 nickel (Gln) (axial ligand) *status experimental F: 257/Modified site: 3'-methylhistidine (His) *status experimental F: 257/Modified site: 5-methylarginine (Arg) *status experimental F: 333/Active site: Tyr *status predicted (Gln) *status experimental F: 446/Rinding site: coenzyme M (Tyr) *status experimental F: 445/Modified site: 1-thioglycine (Gly) *status experimental F: 457/Modified site: 1-thioglycine (Gly) *status experimental F: 452/Binding site: coenzyme B (Asn) *status experimental F: 481/Binding site: coenzyme B (Asn) *status experimental	Query Match  3.4%; Score 99; DB 1; Length 550;  Best Local Similarity 19.5%; Pred. No. 2.6;  Matches 84; Conservative 56; Mismatches 182; Indels 108; Gaps 18;  Qy 141 LRHYQTETHAMSTXNKFFNGFHHSNOWFDRVWYLSVPKSFFEDAYSSGPF 190  11

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21;
                                                                                                                                                                                                                                                                                                                                                                                                                        Teverse transcriptase homolog - sea squirt (Ciona intestinalis)
C;Species: Ciona intestinalis
C;Species: Ciona intestinalis
C;Accession: T31657
R;Bird, A.P.; Clark, V.; Jones, S.J.; Leitgeb, S.; Dobson, R.; Tweedie, S. submitted to the EMBL Data Library, December 1996
A;Reference number: Z21049
A;Reference number: Z21049
A;Accession: T31657
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1209 <br/>
A;Residues: 1-1209 <br/>
BIR>
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C;Genetics:
A;Note: COS41.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    965 VVIQ---CLINLFCL-------FGFPAYVHSDRGLSFISHEVKVFLTERGI 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1006 ATSKSTPYHPQGNSQCER-VNQTIMRTVKLLHGKLMAB-------BQWEEVLPQ- 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313 KG------ANWIPSENILTWIKEEDYEKLVKMARSANMNMIRVWGGGIYEREIFYR 362
                                                                                                                                                                             363 LSAKYPDSFDRYRRPRFDHWGEQAR-----AGNRFYMKTLPMLCQTCQIPMLFTEPGNP 416
    --- AEQN----- GGALFKDLARYG 316
                                                                                         317 IREPKG---WQD---AC-EGKDHI----SHQAWSTFYGFNAASAFHTWVPTEDEMGW 362
                                                                                                                          363 LCDELGIMVWQDFMYACLEYPDHLPWFRKLANBEARKIVRKLRYHPSIVLWC-GNNENNW 421
                                                                                                                                                                                                            196 VSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMT-LGIECIKFLLEQ-- 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INALKLFLQGVTPL-EYLAHRGFAHV-----GRHFTGEGARIAC-QMQSIDEL--RHY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 QTETH----AMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFEDAYSSGPFEF----LTA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 -----DDDNVPIVQRWIDKWFWRGYRLLTIVAMMMDYMQPKRVMSWRESWEMYAEON 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 GGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWLS 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 3.4%; Score 96.5; DB 2; Length 1209; Best Local Similarity 22.9%; Pred. No. 11; Matches 82; Conservative 39; Mismatches 124; Indels 113;
270 RGYRLLTLVAMMMDYMQPKRVMSW--RESWEMY---
                                                                                                                                                                                                                                                                                                                   460 YWPSSPYGGEKAN 472
                                                                                                                                                                                                                                                                      417 ----TKIGARESN 425
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Search completed: September 26, 2000, 20:24:21 Job time: 3645 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

; Search time 92.32 Seconds (without alignments) 387.526 Million cell updates/sec September 26, 2000, 20:28:54 Run on:

US-09-430-029-5 2873

Perfect score: Title:

1 MDTPTLKKKLGLKDRYAAMT.......FDGSEDQKNFAAWRGQATRN 516 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

225878 seqs, 69334122 residues Searched:

225878 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

SPTREMBL\_12:\* Database :

1: sp\_archea:\*
2: sp\_archea:\*
3: sp\_fung::\*
4: sp\_human:\*
5: sp\_nammal:\*
6: sp\_mammal:\*
7: sp\_mhc:\*
8: sp\_organelle:\*
9: sp\_page:\*
11: sp\_ordanel:\*
11: sp\_ordanel:\*
12: sp\_virus:\*
13: sp\_vortebrate:\*
14: sp\_unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	ID	292NP4 Comamonas						032431	043981		Q92455		Q92456	Q9Z458 pseudomonas	292NE2 Comamonas	292459 pseudomonas	030590 burkholderi	295408 pseudomonas	087798 pseudomonas	053007 noderdia oo
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	% Query Match Length DB	536	513	504	372	516	516	511	511	377	381	381	327	205	204	215	169	200	498	10.5
	% Query Match	82.6	80.4	70.6	70.3	64.5	64.4	62.6	62.5	53.7	52.3	52.0	47.1	29.9	29.4	27.7	24.2	13.4	13.1	12.9
	Score	2372	2310.5	2027	2021	1854.5	1849.5	1799	1795	1542	1502	1493	1354	860	844	795	696.5	386	377.5	370
	Result No.	П	7	9	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	10

087082 xanthobacte 069178 alcaligenes 051939 burkholderi 007068 burkholderi		09znl6 unidentifie Q9znl3 unidentifie Q9znl8 unidentifie 006116 methylocyst Q9z4r3 unidentifie 0342r7 uncultured Q9zet3 xanthobacte 053025 nocardia co	1 bovine 2 bovine 1ymantri uncultur burkhold uncultur 2 arabido caenorha
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497 501 501 501	, , , , , , , , , , , , , , , , , , ,	500 600 173 144 141	851 1416 1017 150 329 174 1780
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## ALIGNMENTS

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181 FEDAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMI 240

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                                                                              GWLSAKYPDSFDRYYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKIG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                  1 MDTRVAKKKIGIKERYAAAMTRGIGWETIYQPMDKVFPYDTYEGIKIHDWDKWQDPFRLIM
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                                  AEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEM
                                                                                                                                                          421 ARESNYLGNKFHFCSDHCKDIFDHEPQKYVQAWLPVHQIHQGNCFPPDADPGAEGFDPLA
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                       LGIECIKFLLEQDPDNVPIVQRWIDKWFWRGYRLLTLVAMMMDYMQPKRVMSWRESWEMY
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.4%; Score 2310.5; DB 2;
80.5%; Pred. No. 1.3e-191;
iive 34; Mismatches 65;
                                                                                                                                                                                                                                                                                    513 AA
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Matches 412; Conservative
                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria,
                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                Pseudomonas sp.
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Q52572;
Q1-NOV-1996 (
Q1-NOV-1996 (
O1-NOV-1998 (
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473
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GWLSAKYPDSFDRYYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKIG 420
                       360 OWLSEKYPESFDTLYRPAFEFWARRAEEGRRFYNKTLPMLCTTCOVPMFFTEPGDATKIA 419
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                                                   ARESNYLGNKFHFCSDHCKDIFDHEPQKYVQAWLPVHQIHQGNCFPPDADPGAEGFDPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 KKKLGLKDRYAAMTRGLGWETTYQPMDKVFPYDRYEGIKIHDWDKWVDPFRLTMDAYWKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 RKKINLREKYATMIRDLGWETIYEPMDKVFPFDKYEGIKIHDMDKWEDPFRMIMDAYWKY
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                                                                                                                                                                                                                                                                                                                                                                                        N.;
Ralstonia eutropha strain E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 2027; DB 2; Length 5; Pred. No. 4e-167; 62; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; beta subdivision; Burkholderia
                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                    AA.
                                                                                                       481 AVLDYYAVIMGRDNLDFDGSEDQKNFAAWRGQ 512
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                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                    PRT;
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HINO S., WATANNER K., TAKAHASHI N.
HINO S., WATANNER K., TAKAHASHI N.
Phanol hydroxylase cloned from Ra
novel kinetic properties.";
Microbiology 144:0-0(0).
ERBE, AF026065; AAC32455.1;
SEQUENCE 504 AA, 59270 MW; 6B3
                                                                                                                                                                                                             084961;
01-NOV-1998 (TrEMBLrel. 08, 0
01-NOV-1998 (TrEMBLrel. 08, 1
01-NOV-1998 (TrEMBLRel. 08, 1
PHENOL HYDROXYLASE COMPONENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.6%;
70.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355; Conservative
                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               Ralstonia sp.
                                                                                                                                                                                                                                                                                                                         Ralstonia.
                                                                                                                                                                                                                                                                                                                                                              STRAIN-E2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S:
Matches 355,
                                                                                                                                                                                                   084961
                                                                                                                                                                        ^{\circ}
361
                                                   421
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                                                                                                                                                                                                                                                                                 POXD.
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                                                                                                                                                                        RESULT
084961
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                                                   ŏ
                                                                           g
                                                                                                       QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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Matches 329; Conservative
                                      SEQUENCE FROM N.A.
STRAIN=P35X / NCBI 9869;
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Pseudomonas putida.
                                                                                                                                                                                                                                                                                      Similarity
                                                  AEDLINE; 9512987
                                                                                                                                 DERIVATIVES
                                                                                                                                                                         SIMILARITY)
                   Pseudomonas.
                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                       Best Local
                                                                                                   P35X."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       052164
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                                                                                                                                                                                                            Exhibiting high
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                                                                                                                                                                                                                                                                                                                                                                                                FAHVGRHFTGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSV 176
                                                                                                                                                                                                                                                                                                                                                                                                                            PKSFFEDAYSSGPFEFLTAVSFSFETVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDES 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHMTLGIECIKFILLEQDPDNVPIVQRWIDKWFWRGYRLLTLVAMMMDYMQPKRVMSWRES 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEMYAEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPT 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDEMGWLSAKYPDSFDRYYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNP 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PHENOL HYDROXIAASE ALPHA SUBURIT (FRAGMENT).
Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                         Length 372;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                    STRAIN=E1;
FUTAMATA H., WATANABE K., SUDA F., HARAYAMA S.;
FUTAMATA H., WATANABE K., SUDA F., HARAYAMA S.;
FUTAMATA H., STUTCTUTE found in phenol hydroxylases E affinity towards trichloroethylene.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016861; BAA74746.1;
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PHENOL HYDROXYLASE P3 PROTEIN (EC 1.14.13.7)
(PHENOL 2-MONOOXYGENASE P3 COMPONENT).
                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                      Score 2021; DB 2;
Pred. No. 8.6e-167;
5; Mismatches 2;
                                                                                                                                                                                                                                                                         51167A5D CRC32;
                                                                           372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    516 AA.
                                                                                            01-MAY-1999 (TrEMBLrel. 10, Created)
                                                                           PRT;
    487 AVTMGRDNLDFDGSEDQKNFAAWRG
                274 RINIGADNIDFEGSQDQKNWNAWKG
                                                                                                                                                                                                                                                                        372 AA; 43489 MW;
                                                                                                                                                                                                                                                                                                      70.3%;
98.1%;
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TKIGARESNYLG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 TKIGARESNYLG 372
                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                          Burkholderia.
                                                                                                                                                                                                                                                                                                                         365;
                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         052173;
                                                                        Q9ZNE3
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                                                      RESULT
                                                                Q9ZNE3
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184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 VIKFMLEQHEDNVPIIQRWIDKWFWRGYRLTLIGMMMDYMLPNKVMSWSEAWGYYFEQA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65 KYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGRHF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NG L.C., SHINGLER V., SZE C.C., POH C.L., "Cloning and sequences of the first eight genes of the chromosomally encoded (methyl) phenol degradation pathway from Pseudomonas putida
                                                                                                                                                                                                                                                                                                                                    H(2)O.
-!- COFACTOR: FAD FLAVOPROTEIN, AND REQUIRES FE(+2) FOR ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                     -!- PATHWAY: FIRST STEP OF PHENOL BIODECRADATION.
-!- SUBUNIT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED PO, P1, P2, P3, P4 AND P5 POLYPEPTIDES.
EMBL; X79063; CAA55663.1; -.
EMBL; X79063; CAA55663.1; -.
Flavorite hydrocarbons catabolism; Oxidoreductase; Monooxygenase; Flavoprotein; FAD; Iron.
SEQUENCE 516 AA; 60381 MW; 63E9ED27 CRC32;
                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: PHENOL + NADPH + O(2) = CATECHOL + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 TLKKKLGLKDRYAAMTRGLGWETTYQPMDKVFPYDRYEGIKIHDWDKWVDPFRLIMDAYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 INKKRINIKDKYKYLTRDLGWEPSYQKKEDVFPLEHFEGIKITDWDKWEDPFRLTMDSYW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 TGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFEDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 YSSGPFEFLTAVSFSFEYVLTNILEVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKYPDTFDKYYRPRFEFWREQQAKGERFYNDTLPHLCQVCQVPAIFTEPDDDTKLSLRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 GGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 516;
                                                                                                                                                                                                                                   Gene 151:29-36(1994).
-!- FUNCTION: CATABOLIZES PHENOL, AND SOME OF ITS METHYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.5%; Score 1854.5; DB 2
64.8%; Pred. No. 3.3e-152;
Live 65; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           516 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 YYAVTMGRDNLDFDGSEDQKNFAAWRGQ
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01-JUN-1998 (TrEMBLrel. 06,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 TGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFEDA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                     THKRELLIKDKYRYRITRDLGWEPSYQKKEDVFPLEHFEGIKITDWDKWEDPFRLTMDSYW 62
                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: PHENOL + NADPH + O(2) = CATECHOL + NADP(+) +
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     5 ILKKKLGLKDRYAAMIRGLGWETIYQPMDKVFPYDRYEGIKIHDWDKWVDFFRLIMDAYW 64
                                                                                                                                                                                                                                                           -!- COFACTOR: FAD FLAVOPROTEIN, AND REQUIRES FE(+2) FOR ACTIVITY (BY
                                                                                                                                                                                                                                                                                 PATHWAY: FİRST STEP OF PHENOL BIODEGRADATION.
SUBUNIT: THE MULTICOMPONENT ENZYME PHENOL HYDROXYLASE IS FORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 RTAGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMATVTFGFSAQSDEARHMTLGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 YSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIE
                                                                                                                                                                                                                                                                                                       PO, P1, P2, P3, P4 AND P5 POLYPEPTIDES.

EMBL; X80765; CAA56743.1; -.

Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase;
                                                                      Plasmid pPGH1.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 516;
                                                                                                                                                                                                 MOI. Gen. Genet. 247:240-246(1995).
                                                                                                                                                     HERRMANN H., MUELLER C., SCHMIDT I., MAHNKE J., PETRUSCHKA
                                                                                                                                                                            'Localization and organization of phenol degradation genes
                                                                                                                                                                                                                                                                                                                                                                                                               Indels
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
1-LNOY-1998 (TREMBLRel. 08, Last annotation update)
PHENOL PYDROXYLASE P3 PROTEIN (EC 1.14.13.7)
(PHENOL 2-MONOCXYGENASE P3 COMPONENT).
                                                                                                                                                                                                                                                                                                                                                                                       64.4%; Score 1849.5; DB 2;
64.6%; Pred. No. 8.9e-152;
live 65; Mismatches 106;
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SEQUENCE 516 AA; 60450 MW; 91455AA6 CRC32;
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                                                                                                                                                                                         Pseudomonas putida strain H."
                                                                                                                                                                                                                                                                                                                                                                                                               328; Conservative
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                                                           Pseudomonas putida
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                          MEDLINE; 95272534
                                                                                                                                                                                                                         DERIVATIVES.
                                                                                                                                                                                                                                                                         SIMILARITY).
                                                                                               Seudomonas.
                                                                                                                                                                  HAHNKE K.;
                                                                                                                                STRAIN-H;
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Matches 32
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307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 GARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFEDAYSS
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                                                                                                                                                                                                                                                      MEDLINE; 98005684.

HORINOUCHI M., KASUGA K., NOJIRI H., YAMANE H., OMORI T.;

"Cloning and characterization of genes encoding an enzyme which
oxidizes dimethyl sulfide in Acinetobacter sp. strain 20B.";

FEMS Microbiol. Lett. 155:99-105(1997).

EMBL; D85083; BAA23333.1; --
SEQUENCE 511 AA; 60332 MW; CC36C8CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
                                                                                                                                                                       gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 511;
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01, Last sequence update)
08, Last annotation update)
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Last annotation update)
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Pred. No. 2e-147;
59; Mismatches 112;
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                                                                                                                                                                                        Moraxellaceae; Acinetobacter
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                                                                                                                                                                       Bacteria; Proteobacteria;
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                                                                                                                    DMS OXYGENASE COMPONENT
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Q43981,
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377 AA; 44269 MW;
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381 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                  STRAIN-NCIB6200,
MEDLINE; 96154937.
MEDLINE; 96154937.
EHRT S., SCHIRMER F., HILLEN W.;
"Genetic organization, nucleotide sequence and regulation of expression of genes encoding phenol hydroxylase and catechol 1,2-dioxygenase in Acinetobacter calcoaceticus NCIB8250.";
Mol. Microbiol. 18:13-20(1995).
EMBL; 236909; CAA85383.1; -... 511 AA; 60316 MW; DAOF2BCE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFEDAYSS
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                   Acinetobacter calcoaceticus.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
Moraxellaceae; Acinetobacter.
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                                                                                                                                                                                                                                                                                                                                              62.5%; Score 1795; DB 2; Length 51.
64.1%; Pred. No. 4.5e-147;
ive 60; Mismatches 112; Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
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STRAIN=P-10;
FUTAMATA H:, WATANABE K., SUDA F., HARAYAMA
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    PHENOLHYDROXYLASE COMPONENT.
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Best Local Simil
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Q92454;
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"Unique primary structure found in phenol hydroxylases Exhibiting high affinity towards trichloroethylene.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AB016860; BAA745.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUTAWATA H., WATANABE K., SUDA F., HARAYAWA S.;
"Unique primary structure found in phenol hydroxylases Exhibiting high affinity towards trichloroethylene.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016859; BAA74744.1;
                                                                                                                                                                                                                                                                                                                63 YWKYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGR 122
                                                                                                                                                                                                                                                                                                                                                                                                             123 HFTGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                         243 IECIKFLLEQDPDNVPIVQRWIDKWFWRGYRLLTLVAMMMDYMQPKRVMSWRESWEMYAE 302
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGW 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSAKYPDSFDRYYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKIGAR 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DAYWKYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 DAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHWTLG
                                                                                                                                                                                                                                                                          0;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TEMBLrel. 12, Last annotation update)
PHENOL HYDROXYLASE ALPHA SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                      ; Score 1542; DB 2;
; Pred. No. 2.1e-125;
46; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.3%; Score 1502; DB 2;
ilarity 70.3%; Pred. No. 6.1e-122;
Conservative 44; Mismatches 69;
                                                                                                                                                  7B66BF49 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44420 MW; 6B2A25F1 CRC32;
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241 FEEAGGALFKDLERYGIRPPKHVEEANIAKDHVSHQAWSIFYQYSQATNFHTWMPTDEEL 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   365 AKYPDSFDRYYRPRFDHWGEQARAGNR 391
                                                                                                                                                                                           Created)
                                                                                                                                                                 PRT;
                                                                            421 ARESNYLGNKFHFCSDHCKDI 441
                                                                                          361 HRSTEHEGERYHFCSQGCCDI 381
                                                                                                                                                                                                                                                                                                                                                                                                          38388 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              327
327 AA;
                                                                                                                                                                                                                                            Pseudomonas putida.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=P-6;
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SEQUENCE
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Matches 244
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Q9Z458
ID Q9Z458
AC Q9Z458;
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                                                                                                                                                                  092456
                                                                                                                                           RESULT
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FUTAMATA H., WARANABE K., SUDA F., HARAYAMA S.;
FUTAMATA H., WARANABE K., GUDA F., HARAYAMA S.;
"Unique primary structure found in phenol hydroxylases Exhibiting high
affinity towards trichloroethylene.",
SUDMILITED (ACC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016857; BAA74742.1; -.
EMBL; AB016854; BAA74739.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSIFYGFNAASAFHTWVPTEDEM 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LGIECIKFLLEQDPDNVPIVQRWIDKWFWRGYRLLTLVAMMMDYMQPKRVMSWRESWEMY 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAYWKYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRQFSGAGARIACQMQAIDELRHVQTQIHAMSHYNKHFNGLHDFAHMHDRVWFI,SVPKSF 120
                                                                                                                                                                                   301 DWLSSKYPDTFDKIYRPRYEHWRALQEKGERFYNPTLPMLCQICQIPLAFGEPDDPTTLS 360
                               LGIECIKFLLEQDPDNVPIVQRWIDKWFWRGYRLLTLVAMMMDYMQPKRVMSWRESWEMY 300
                                                                                                                                                                    301 AEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEM 360
                                                                                                                                                                                                                    361 GWLSAKYPDSFDRYYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKIG 420
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                                                                                                                                            LGLEVIKFLLEQHEDNVPIIQRWIDKWFWRGYRLLTLVGMMMDYMLPNKVMSWSEAWGVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
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                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.0%; Score 1493; DB 2; 70.1%; Pred. No. 3.7e-121; Live 43; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44525 MW; 5591FE88 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAX-1999 (TrEMBLrel. 10, Last sequence upc
01-WAY-1999 (TrEMBLrel. 12, Last annotation up
PHENOL HYDROXYLASE ALPHA SUBUNIT (FRAGMENT).
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381 AA;
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Matches 267; Conserv
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SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
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FUTANATA H., WATANABE K., SUDA F., HARAYAMA S.;
"Unique primary structure found in phenol hydroxylases Exhibiting high affinity towards trichloroethylene.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016858; BAA74743.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GGALFKDLERYGIRPPKYVEQTTIGKEHISHQAWSIFYQYSQATNFHTWIPTDEELDWLS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 CIKFILLEQDPDNVPIVQRWIDKWFWRGYRLLTLVAMMMDYMQPKRVMSWRESWEMYAEQN 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWLS 364
                                                     301 DWLSSKYPDTFDKIYRPRFEHWRALQEKGERFYNPTLPMLCQICQIPLSFGEPDDQTTLS 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 KYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGRHF 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 TGEGARIACOMOSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFEDA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 YSSGPFEFLTAVSFSFEYVLTNLLEVPFMSGAAYNGDMSTYTFGFSAQSDESRHMTLGIE
361 GWLSAKYPDSFDRYYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group; Pseudomonas.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PHENOL HYDROXILASE ALPHA SUBUNIT (FRAGMENT).
Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                                     1999 (TrEMBLrel. 10, Last Sequence update)
-1999 (TrEMBLrel. 12, Last annotation update)
HYDROXYLASE ALPHA SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47.1%; Score 1354; DB 2; 74.6%; Pred. No. 3e-109; tive 31; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFF0A7B0 CRC32;
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121 PKSFFDDAFTAGPFEFMIAIGFAFEYVLTNLLFVPFISGAAYNGDMGAMAFGFSAQSDES 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: September 26, 2000, 20:28:57 Job time: 1016 sec
                                                                                                                   PRT;
                                          181 RHMTLGLEIIKFILEQDPDNLPIV
                            237 RHMTLGIECIKFLLEQDPDNVPIV
                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 27.7%
Best Local Similarity 64.0%
Matches 137; Conservative
                                                                                                                   PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                   Pseudomonas.
                                                                                                                 Q9Z459
                                                                                         RESULT 15
Q9Z459
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                                                          FUTAMATA H., WATANABE K., SUDA F., HARAYAMA S.;
"Unique primary structure found in phenol hydroxylases Exhibiting high
affinity towards tribliorocthylene.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016856; BAA74741.1; -.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-E6;
FUTAMATA H., WATANABE K., SUDA F., HARAYAMA S.;
Unique primary structure found in phenol hydroxylases Exhibiting high affinity towards trichloroethylene.",
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016862; BAA74747.1; -.
                                                                                                                                                                                                                                                                                                Comamonas sp.
Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
                                                                                                                                                                                                                                   55 PFRLTMDAYWKYQGEKEKKLYAVIDAFIQNNAFLGVSDARYINALKLFLQGVTPLEYLAH 114
                                                                                                                                                                                                                                                                                   115 RGFAHVGRHFTGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYL 174
                                                                                                                                                                                                                                                                                                                                   175 SVPKSFFEDAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSD 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 RLTMDAYWKYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRG 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 FAHVGRHFTGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSV 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PKSFFEDAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDES 236
                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                9
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0
                                                                                                                                                                                      Length 205;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PHENOL HYDROXYLASE ALPHA SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.4%; Score 844; DB 2; L. 74.0%; Pred. No. 1.8e-65; Live 27; Mismatches 26;
                                                                                                                                                                                     29.9%; Score 860; DB 2; 78.5%; Pred. No. 7.6e-67; Live 17; Mismatches 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204 204
204 AA; 23298 MW; DB5A9322 CRC32;
                                                                                                                                                 205 AA; 23441 MW; E19D7C89 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                    235 ESRHMTLGIECIKFLLEQDPDNVPI 259
                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 29.9%
Best Local Similarity 78.5%
Matches 161; Conservative
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 74.0%
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                      205
                                     SEQUENCE FROM N.A.
              seudomonas.
                                                                                                                                    NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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STRAIN-P-1:
FUTAMATA H., WATANABE K., SUDA F., HARAYAMA S.;
SUTAMATA H., WATANABE K., SUDA F., HARAYANABE EXHIBITING high affinity towards trichloroethylene.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016855; BAA74740.1;
NOW_TER 1 1 1
NOW_TER 215
SEQUENCE 215 AA; 25713 MW; AEBD075A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 SDESRHMTLGIECIKFLLEQDPDNVPIVQRWIDKWFWRGYRLLTLVAMMMDYMQPKRVMS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WVPTEDEMGWLSAKYPDSFDRYYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTE 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 WRESWEMYAEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.7%; Score 795; DB 2; Length 215; 64.0%; Pred. No. 3.3e-61; live 29; Mismatches 48; Indels
                                              01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PHENOL HYDROXYLASE ALPHA SUBUNIT (FRAGMENT).
215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGNPTKIGARESNYLGNKFHFCSDHCKDIFDHEP 446
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GenCore version 4.5
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OM protein - protein search, using sw model

September 26, 2000, 20:11:44 ; Search time 75:19 Seconds
(without alignments)
162.549 Million cell updates/sec Run on:

US-09-430-029-5 2873 1 MDTPILKKKLGLKDRYAAMT......FDGSEDQKNFAAWRGQATRN 516 ritle:
Perfect score:
Sequence:

Scoring table:

188963 seqs, 23686106 residues BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

0		Description		$\Box$	Nocardia corallina			Nocardia corallina	ylase	Bacillus sp. alpha	Bacillus sp. alpha	Arabidopsis thalia	Plasmid pTUB613 he	Plasmid pTUB616 he	Thermotoga maritim	Human angiotensin	Streptococcus pneu	Human 1(3)mbt prot	Human 1(3)mbt prot	Lys-aminopeptidase	Human angiotensin	B. stearothermophi	An alpha-amylase (	Protein encoded by	Mouse 1(3)mbt prot	Muramidase release	Protein sequence o	Alpha-amylase gene	Aminopeptidase H11	Glycosyltransferas	Aspergillus niger	Bacillus stearothe	Bacillus stearothe	stearoth	Lysine decarboxyla
SUMMARIES		QI .	W06802	W98973	R66215	R81471	R66213	R81469	W12955	W31502	W48263	W59446	P70579	P70580	W49873	R04111	W69165	Y01070	Y01069	R67760	W68155	W39744	Y01585	W71249	Y01071	R27746	W71251	P70338	R58701	R42995	221	R78269	244	14	R99797
		DB																															Н		
		Length		504	501	501	342	343	514	515	515	526	572	559	684	1306	1965	738	772	843	1306	548	548	485	826	1256	217	549	962	985	985	514	515	515	713
o <del>l</del>	Query	Match	im	0		12.9				3.6																							3.1		
		Score		2027	370	370	115	109	104	104	104	103	102	66	98.5	94.5	94	93.5	93.5	92.5	92.5	91.5	91.5	91	91	90.5	06	90	89.5	89.5	89.5	88	88	88	88
	Result	No.	1	7	8	4	5	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

Alanyl-tRNA synthe	Helminth aminopept	Aspergillus oryzae	Aspergillus oryzae	Rat 1(3)mbt protei	Human c-IAP2. Nucl	Human inhibitor of	Tobacco leaf antif	Tobacco leaf antif	Sequence of the al	Yeast NPC1 protein
W21898	R51280	W89589	M97798	X01072	W13546	W19747	R78680	R78679	P70376	WB8447
		Н	٦	Н	Н	<del>, -</del>	Н	П	-	٦
876	972	771	771	826	604	604	518	540	529	1170
3.0	3.0	3.0	3.0	3.0	2.9	2.9	2.9	2.9	5.9	2.9
87	86.5	98	98	85.5	84.5	84.5	84	84	83.5	83.5
34	9 9 9 9	37	38	36	40	41	42	43	44	45

## ALIGNMENTS

		e o :-t	0;				
		O D	Gaps	60	120	180	240
	pollutant;	00-ANGY-1996. 00-ANGY-1991; 694718. 02-MAY-1991; 05-694718. 02-MAY-1991; US-694718. 11-DEC-1993; US-167457. 02-CCT-1994; US-19387. 11-DEC-1994; US-319387. 11-DEC-1994; US-319387. 11-DEC-1994; US-319387. 12-DEC-1994; US-319387. 13-DEC-1994; US-319387. 14-DEC-1994; US-319387. 15-DEC-1994; US-319387. 15-DEC-1994. 15-DEC-1994; US-319387. 15-DEC-1994. 15-DEC-1	0; 6	DPFRLTM 	GFAHV     :  GFAHI	VPKSF 	SRHMT
		enzyme nd aron nd aron nd aron issabl lloroetiloroetismissal smissab be gen tors o ' prors induc	n 519; Is	OKWVDP          OKWEDP	EYLAHK   :    EYMAHF	RVWYLS	SAQSDE
	eactor	Tom (ds. al cooxygue cooxygue)  Transmittrich transit can can cooreac coortg	Length Indels	KIHDW       KIHDW	GVTPL         GVTPL	SNOWFD    :  SIHWYD	IVTEGE 
	; bior Lon.	PR1-23 Tom tic cpds. e ho-monooxyc domonas cey self-transis self-transis ading tricl mid is trai cteria can in bioreac trai cont (TL-23 cont able of ful require an	B 1; -241; 45;	DRYEG]  :     DKYEG]	LKLFL   : :   KVFL	NGFHHS     :	NGDMS
	tomA3. :itutive legradat:	cepacia h. uene ort uene ort rrom Pseu a large of degr many ba cE, esp. espacia P	19; D 5.9e cches	OKVEPY SKVEPY	ARY INA    :   ARY VNA	IYNKEE    :1 HYNKYE	MSGAAY
	it nst	06-MAY-1991; 694718.  02-MAY-1991; 694718.  15-DEC-1993; US-694718.  15-DEC-1993; US-167457.  06-OCT-1994; US-319387.  (FRAM.) FRANCESCONI S C.  (SHIE/) SHIELDS M S.  Francesconi S.C. Shields MS;  Francorganisms transformed with P. cepacia FR1-23 Tom enzyme are useful for degradation of chloro:allphatic cpds. and aro claim 1; Column 29-32; 25pp; English.  N-PSDB; T44457.  N-PSDB; FRANCESCONI S C.  The present sequence is that of toluene ortho-monoxygenase toma3 encoded by T44457, isolated from Pseudomonas cepacia stoma3 encoded by T44457, isolated from Pseudomonas cepacia coma3 encoded by T44457, isolated from Pseudomonas cepacia SFR1-3. The Tom gene is present on a large self-transmissable denoted prom. The enzyme is capable of degrading trichloroet (TCB), a hazardous pollutant. The promy bacteria can be generated to constitutively degrade TCB, esp. in bioreactors of altered to constitutively degrade TCB, esp. in bioreactors of the expressable in other bacteria, thus many bacteria can be gen altered to constitutional inducers and is capable of functionined exogenous chemical inducers and is capable of functionined consubstrate for the enzyme required to break down TCE, in experiments.	Subject to competitive initialition.  (ence 519 AA; latch 83.88; Score 2409; DB 1; cal Similarity 81.88; Pred. No. 5.9e-241; cal 419; Conservative 48; Mismatches 45;	MDTPTLKKKLGLKDRYAAMTRGLGWETTYQPMDKVFPYDRYEGIKIHDWDKWVDFFRLTM	DAYWKYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGYTPLEYLAHKGFAHV 	GRHFTGEGARIACQMOSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSF 	FEDAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMT 
519 AA	s subunit ole; const ne; TCE; d PR1-23.	S; with of ch of ch of ch select select select select select degrad degrad futs. F dants. F	SCC; Pre	GLGWET     :   GLGWQT	TONNAF              -	RHYOTE   :    RHFQTE	YVLTNI
	W068U2; UJAN-1997 (first entry) TOluene ortho-monooxygenase subun. tom; pTOM; self-transmissable; colbreakdown; trichloroethylene; TCE Pseudomonas cepacia strain PR1-23 USS543317-A.	4718694718167457167457167457167457	83.8%; 81.8%; sive 4	CAAMTR	AVIDAE        AVIDAE	SIDEL          SIDEL	VSFSFE
Protein;	(first e -monooxy lf-trans ichloroe epacia s	9996. 991, US-694718. 991; US-694718. 993; US-167457. 994, US-319387. 994, US-319387. SHIELDS M S. SHIELDS M S. 370640/27. T44457. Tanisms transformu 29-32, 22 clumn 29-32, 22 clumn 29-32, 22 cent sequence is rocoded by T44457. The Tom gree is prow. The enzyme the constitutivel aminated environ seque for constitutivel constitutivel constitutivel constitutivel set of condition set of condition set for the enz	to competiti (19 AA; 83. larity 81. Conservative	GLKDRY        GLKDRY	EKKLY? 	IACOM( :     VACOM(	EFLTA
standard;	7 (fi tho-mc self- trich s cepe	0.6-AUG-1996. 0.2-MAY-1991; 0.5-694 0.2-MAY-1991; 0.5-694 15-DEC-1993; 0.5-167 16-DEC-1994; 0.5-319 (FRAN,) FRANCESCONI (SHIE/) SHIELDS M S FRANCESCONI SC, Sh WPI: 96-370640/37. N-PSDB; T44457. N-PSDB; T44457. N-PSDB; T44457. The present sequenc Claim 1; Column 29- The present sequenc Claim 2; The Tom gen denoted prom. The e (TCB), a hazardous expressable in othe altered to constitut TCB-contaminated en need exogenous chem diverse set of cond diverse set of cond constitut constitut constitut constants for the	519 AA; 519 AA; milarity Conser	LLKKKL       70KKKL	CYQGEK         CYQGEK	GEGAR         GEGAR	rssgpf :
	W06802; 29-JAN-1997 Toluene orth tom; PTOM; s breakdown; t Pseudomonas US5543317-A.	06-AUC-1996. 02-MAY-1991; 69 02-MAY-1991; 69 02-MAY-1991; 60 06-OCT-1994; US 06-OCT-1994; US (FRAN/) FRANCES (SHIE/) SHIELDS (TABANCES CLAIM 1; COLUMN The present seq troma3 encoded by present seq troma3 encoded by Tromas ancoded by CTCB), a hazard denoted prom. The Tomas ancoded by Tromas ancoded b	not subject Sequence ry Match t Local Sir ches 419;				
LT 1 02 W06802	W06802; 29-JAN- Toluene tom; pT breakdc Pseudom US55433	06-AUG- 02-MAY- 02-MAY- 15-DEC- 66-OCI (FRAN/) (SHIE/) (SHIE/) (SHIE/) (SHIE/) MICROOF MICROOF MICROOF MICROOF AID DE CIAIM J GADOLEG AID COOR AID	not subject to compose Sequence 519 AA; Sequence 519 AA; Query Match Best Local Similarity Matches 419; Conserv	п т ;	61	121	181
RESULT W06802 ID W	AC DE KW KW OS	PP P P P P P P P P P P P P P P P P P P	200 200 200 200 200 200 200 200 200 200	Qy Db	OY Db	QY Db	Qy

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244 KFICEQDPDNIPILQKWLDKWFWRGFRLLTLVGMMMDYMLPRRVMSWAEAWEMYFEQAGG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alkene mon:oxygenase and corresp. gene - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.9%; Score 370; DB 1; 25.6%; Pred. No. 7.9e-30;
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from NADH coenzyme to a monoxygenase.
Sequence 501 AA;
                                                                                                                                                                                                                                                                                                            487 AVIMGRDNLDFDGSEDQKNFAAWRG 511
                                                                                                                                                                                                                                                                                                                                         474 RENEGADNEDFEGSQDQKNWNAWKG 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein; 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.OCT-1994.
06-APR-1993; 105171.
06-APR-1993; JP-105171.
(NIHA ) JAPAN ENERGY CORP.
WPI; 95-009069/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 PYDRYEGIKIHDWD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nocardia corallina.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; Q79569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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R66215;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New encoding an aromatic cpd. oxidative decompsn. enzyme - useful in the fields of petroleum purification, chemical and drug industries Claim 1: Page 7-19: 35pp; Japanese.

The present sequence encodes Alcaligenes sp. protein PoxD. The present invention also describes PoxA, PoxB, PoxC, PoxR, PoxE, PoxF, PoxF, PoxE, and PoxI. The proteins are useful in the fields of petroleum purification, chemical industry and drug industry related to the synthesis, conversion and decomposition of aromatic compounds.
181 FEDAATGGPFEFLIAVSFSFEYVLINLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMT 240
                                                                                                                                                  PoxD; PoxE; PoxF; PoxG; PoxH;
purification; chemical industry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGRHFTG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127 EGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFEDAYS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGPFEFLTAVSFSFEYVLINLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIECI 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KFLLEQDPDNVPIVQRWIDKWFWRGYRLLTIVAMMMDYMQPRRVMSWRESWEMYAEONGG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 KKKLGLKDRYAAMTRGLGWETTYQPMDKVFPYDRYEGIKIHDWDKWVDFFRLTMDAYWKY 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                         LGIECIKFILEQDPDNVPIVQRWIDKWFWRGYRLLILVAMMMDYMQPKRVMSWRESWEMY
                                                                 AEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEM
                                                                                                                                                                                                          361 GWLSAKYPDSFDRYYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNPTKIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.6%; Score 2027; DB 1; Length 504; 70.3%; Pred. No. 2e-201; ...ve 62; Mismatches 78; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                            481 AVLDYYAVTMGRDNLDFDGSEDQKNFAAWRGQ 512
                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-1999 (first entry)
Alcaligenes sp. protein PoxD.
Alcaligenes; PoxR; PoxA; PoxB; PoxC;
PoxI; aromatic; oxidative; petroleum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W98973 standard; Protein; 504
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25-JUL-1997; JP-200625.
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WPI; 99-197820/17.
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                                                                                  241
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W98973
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21;
                                           LGNKFHFCSDHCKDIFDHEPQKYYQAWLPVHQIHQGNCFPPDADPGAEGFDPLAAVLDYY 486
                                                                                                                                                                                                                                                                                                                             -----GGASLEDVLKWY 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epoxidation of an alkene Claim 1: Page 3-4; 30pp; Japanese. E.coli transformed with the DNA sequence 0/9569 are able to E.coli transformed with the DNA sequence 0/9569 are able to catalyse the epoxidation of alkenes. The DNA is derived from Nocardia corallina and comprises 4 open reading frames. ORFs amoA and amoC encode subunits 1 and 2 of the alkene monoxygenase enzyme and ORF amoD encodes a reductase capable of transferring electrons
ALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWLSAK
                                                                                                                       367 YPDSFDRYYRPRFDHWGEQARAGNRFYMKTLPMLCQTCQIPMLFTEPGNPTXIGARESNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTQLHEKSKSYDWDFTSVERRPKFETKYKMPKKGKDPFRVLIRDYMKMEAEKDDRTHGFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGAVRTREATRI-EPRFAEAMKIMVPQLTNAEYQAVAGCGMIISAVENQELRQGYAAQML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 TLGIECIKFLLEQDPDNVPIVQRWIDKWFWRGYRLL-TLVAMMMDYMQPKRVMSWRESWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 DELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 -FEDAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 ANGYGSVMALLIENE-DNLPLLNQSLDRHFWRAHKALDNAVGWCSEYGARKRPWSYKAOWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYAEQN--GGALFKDLARYGIREPKGWQDACEG-----KDHISHQAWSTFYGFNAAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nocardia corallina alkene monoxygenase subunit-2. alkene monoxygenase; subunit-2; epoxidation; amoC.
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21;
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R81469-R81472 are protein products of the Nocardia corallina strain
B-276 alkene mono-oxygenase gene. The gene encodes 4 protein products
amoA, amoC and amoD derived from the 3 different reading frames
of the operon. The gene is useful for the production of indigo via
contg. indole and will readily oxidise the indole yielding indigo into
the culture medium. E. coli may also be transformed with the alkene
by microbial oxidation.
349 AFHTWVPTEDEMG-----WLSAKYPDSFDRYYRPRFDHW-GEQA----RAGNRFYMKTLPM 399
                                                                                   389 LPPMCQVCQVPCVMP---RLDMNAARIIEFEGGKIALCSEPCQRIFTNWPEAYRHRKQYW 445
                      ---FW--RSDAMGPADFEWFENHYPGWSAAYQ----GYWEGYKALADPAGGRIMLQELPG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 DAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGRHFTGEGARIACQMQSI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 DEVRHAQLE---MTLRN-----YYAKHWCD-----PSGFDIGQRGLYQHPAGLVSIG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 TLGIECIKFLLEQDPDNVPIVQRWIDKWFWRGYRLL-TLVAMMMDYMQPKRVMSWRESWE 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---KWVDPFRLTMDAYWKYQGEKEKKLYAVI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIQLHEKSKSYDWDFTSVERRPKFETKYKMPKKGKDPFRVLIRDYMKMEAEKDDRTHGFL 64
                                                           400 L---CQTCQIPMLFTEPGNPTKIGARESNYLGNKFHFCSDHCKDIFDHEPQKY---VQAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Prepn. of indigo by a microbiological method - by culturing a microbe having alkene monooxygenase activity to oxidise indole to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -FEDAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHM
                                                                                                                                                                                                                                                     R81411;
07-A06-1996 (first entry)
Nocardia corallina alkene mono-oxygenase gene product, amoC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.9%; Score 370; DB 1; Length 501;
25.6%; Pred. No. 7.9e-30;
tive 68; Mismatches 190; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                         /note= "Trp residue given in the specification corresponding to a TCG codon in T17418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 DELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSF---
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
misc_difference 268
                                                                                                                                                                                                                               R81471 standard; Protein; 501 AA.
                                                                                                                                                                                                                                                                                             Alkene mono-oxygenase; indole;
microbial oxidation; dye.
Nocardia corallina B-276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-1994; JP-179688
(NIHA ) JAPAN ENERGY CORP.
WPI; 96-133426/14.
N-PSDB; T17418.
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                                                                                                                                                          446 ARYH 449
                                                                                                                          454 LPVH 457
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Best Local Simi
Matches 124;
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228 ANGYGSVMALLENB-DNLPLLNGSLDRHFWRAHKALDNAVGWCSEYGARKRPWSYKAQWE 286

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---KDHISHQAWSTFYGFNAAS 348
                                                                                                                                                                                                                                                                                                        44 IKIHDWDKWVDFFRLTMDAYWKYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----EYLAHRGFAHVGRHFTGEGARIACQMQSIDELRHYQTE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 -AITPIWSOKILARSYAAWPFVEYGLFLSLAYAVROAMSDTVQFSVVFQAVDRMRLLQDI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288
                                                         ---WLSAKYPDSFDRYYRPRFDHW-GEQA---RAGNRFYMKTLPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claim 1; Page 2; 30pp; Japanese.
E.coli transformed with the DNA sequence 079569 are able to E.coli transformed with the DNA sequence 079569 are able to catalyse the epoxidation of alkenes. The DNA is derived from Nocardia corallina and comprises 4 open reading frames. ORFs amoh and amoc encode subunits 1 and 2 of the alkene monoxygenase enzyme and ORF amob encodes a reductase capable of transferring electrons
                                                                                                                                                                                            ---FW--RSDAMGPADFEWFENHYPGWSAAYQ----GYWEGYKALADPAGGRIMLQELPG
                                                                                                                                                                                                                                                            L---CQTCQIPMLFTEPGNPTKIGARESNYLGNKFHFCSDHCKDIFDHEPQKY---VQAW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLLFVP-FMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIECIKFLLEQDP----DNVPIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.0%; Score 115; DB 1; Length 342; 19.8%; Pred. No. 0.0011; tive 39; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 VRISEWSAYRDPHQLWQRPYVSTCNQDQQALARLVPVLIMGSA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nocardia corallina alkene monoxygenase subunit-1. alkene monoxygenase; subunit-1; epoxidation; amoA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alkene mon:oxygenase and corresp. gene - useful for the
299 MYAEQN--GGALFKDLARYGIREPKGWQDACEG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from NADH coenzyme to a monoxygenase. Sequence 342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R66213 standard; Protein; 342 AA.
                                        : : | : : |: : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | :
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(NIHA ) JAPAN ENERGY CORP.
WPI; 95-009069/02.
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                                                                                                                                   349 AFHTWVPTEDEMG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nocardia corallina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 QGVTPL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 QRWIDKW 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; Q79569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epoxidation of
                                                                                                                                                                                                                                                                                                                                                                                            454 LPVH 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                            446 ARYH 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J06292571-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRWIEEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R66213;
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                                                                                                                                                                                                                                                                400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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R81469
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                                                                                                                                                                                                                                                            QY
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                                                                                                                                                                                                                                                                                                                                                                                            δλ
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12-SEP-1997.
04-MAR-1997; U03635.
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                          514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 IKF---
                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ထ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha-amylase. detergent; thermal stability; oxidation stability; enzyme; blpha-amylase; detergent; alpha-amylolytic activity; washing composition; calcium ion dependency; alpha-amylolytic activity; washing composition; textile desizing; papermaking; beer-making; ethanol production;
                                                                                                                                                                                                         claim 5, Page 6-7; 11pp; Japanese. It he Nocardia corallina strain R81469-R81472 are protein products of the Nocardia corallina strain B-276 alkene mono-oxygenase gene. The gene encodes 4 protein products amon, amoc, and amo derived from the 3 different reading frames of the operon. The gene is useful for the production of indigo via oxidation of indole. Nocardia corallina can be cultured in a medium contg. Indole and will reading voxidise the indole yielding indigo into the culture medium. E. coli may also be transformed with the alkene mono-oxygenase gene and used as above to efficiently produce indigo by microbial oxidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 -AITPIWSQKILARSYAAWPFVEYGLFLSLAYAVROAMSDTVQFSVVFQAVDRMRLLQDI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 VHHLDHLOESPEFSDAGAREAWASDSTLVPIREVIERIAASQDWVEILVAGTLVFEPLVG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          260
                                                                                                                                                                                                                                                                                                                                                                                                                                            44 IKIHDWDKWVDPFRLTMDAYWKYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QGVTPL-------EYLAHRGFAHVGRHFTGEGARIACQMQSIDELRHYQTE 147
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 THAMSTYNKF--FNGFHHSNQWFDRVWYLSVPKSFFEDAYSSGPFEFLTAVSFSFEYVLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NELFVP-FMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIECIKFLLEQDP----DNVPIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          microbe having alkene monooxygenase activity to oxidise indole to
                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                           Nocardia corallina alkene mono-oxygenase gene product, amoA. Alkene mono-oxygenase; indole; indigo production; biosynthesis; microbial oxidation; dye.
                                                                                                                                                                         Prepn. of indigo by a microbiological method - by culturing
                                                                                                                                                                                                                                                                                                                                                                                         Length 343;
                                                                                                                                                                                                                                                                                                                                                                                         3.8%; Score 109; DB 1; Length 34 19.4%; Pred. No. 0.0047; tive 39; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 VRISEWSAYRDPHQIMQRPYVSTCNQDQQALARLVPVLIMGSA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W12955 standard; protein; 514 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus stearothermophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-FEB-1995; DK-000126.
29-KAK-1995; DK-000336.
29-SEP-1995; DK-001097.
06-0CT-1995; DK-001121.
(NOVO ) NOVO-NORDISK AS.
        R81469;
07-AUG-1996 (first entry)
                                                                                                30-JAN-1996.
08-JUL-1994; 179688.
08-JUL-1994; JP-179688.
(NIHA ) JAPAN ENERGY CORP.
WPI; 96-133426/14.
                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 19.4 Matches 48; Conservative
                                                                       Nocardia corallina B-276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-1996; DK0056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              290 RRWIEEW 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRWIDKW 267
                                                                                                                                                                   N-PSDB; T17418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09623873-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-AUG-1996
                                                                                      J08023988-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sweetener.
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W12955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W12955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
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24;
                                                                                                                                                                                                                                                          strearchermophilus. The variants of the invention were created using strearchermophilus. The variants of the invention can have improved parent alpha-amylases. The variants of the invention can have improved thermal stability (such as at temperatures in the range of 40-70 degrees thermal stability (such as at temperatures in the range of 40-70 degrees celcius), and/or oxidation stability, and/or reduced calcium ion dependency. The variants can also have increased alpha-amylases are sepecially at ph values in the range of 8.5-10.5, and improved binding of a particular substrate. The variants also possess improved specificity to a particular substrate, and/or improved specificity with respect to cleavage of substrate. The variants can be used in detergent and washing compositions, and for textile can be used in detergent and washing compositions, and for textile desizing. The alpha-amylase variants of the invention can also be used in papermaking and beer-making processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 YAEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVP---T 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 440 VGKQHAGKVFYDLT--GNR----SDTVT----INSDGWGEF-KVNGGSV-SVWVPRKTT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             323 ---AVTEVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGYPCVFYGDYYGIPQYNIPS 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 KGIGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKSWGKWYVNTTNIDGFRLDAVKH 238
                                                                                                                       Disclosure; Page 86-88; 111pp; English. W12955, W12956, R81835 and R81836 represent the parent alpha-amylases used to create the variants of the invention (such as W12098-W12131). This sequence represents the alpha-amylase from Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VDPFRLTMDAY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 WKYQGEKEKKLYAVIDAFTQNNAFL--GVSDARYINALKLFLQGVTPLEYLAHRGFAHVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --SFFPDWLSDVRSQTGKPLFTVG----EYWSY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 RHFTGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 EDAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 104; DB 1; Length 514;
Pred. No. 0.029;
3; Mismatches 125; Indels 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-APR-1998 (first entry)
Bacillus sp. alpha amylase.
Alpha amylase; hard surface cleaning; dishwashing; laundry.
Bacillus sp.
W09732961-A2.
                                                        Alpha-amylase variants - with improved thermal and oxidation stability and reduced calcium ion dependency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       beer-making processes. The variants of the invention the production of sweeteners and ethanol from starch.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 TASKSGGTEDMRT-----LMTNTLM------KDQPTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 GIECIKFLLEQDPDNVPIVQRWIDKWF-------WRGYRLL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 RGLG--WETTYQPMDKVFPYDRYEGI------KIHDWDKW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269 ------DINKLHNYIMKTN--GTMSLFDAPLHN-
Svendsen A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276 -----TLVA-----MMMDYMQPKRVMSW-RE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           357 EDEMGWLSAKYP--DSFDRYYRPRFDHW 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          487 VSTIAWSITTRPWTDEFVRWTEPRLVAW 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W31502 standard; protein; 515 AA.
W31502;
Bisgard-frantzen H, Borchert T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.6%;
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EDEMGWLSAKYP--DSFDRYYRPRFDHW 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 VSTIAWSITIRPWIDEFVRWIEPRLVAW 514
                                                                                                                                                                                                      21 RGLG--WETTYQPMDKVFPYDRYEGI-----
                                                                                                                                                                                                                                                                                                                                                                                                                              GIECIKFLLEQDPDNVPIVQRWIDKWF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-0cT-1996 (first entry)
Arbidopsis thaliana MLO protein h
MLO; mildew; pathogen; resistance.
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Fig 15; 150pp; English.
                                                                                                                                                                            43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W59446 standard; Protein; 526
                                                                                                                                                3.6%;
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JUL-1997; G02046.
07-MAR-1997; GB-004789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1996; GB-015879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-OCT-1996; GB-022626
                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-FEB-1998.
                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W59446;
                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
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        δŏ
                                                                                                                                                                                                                                                                                    qq
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                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                               qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΫ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alpha amylaše protein #3.
2; stain digestion; detergent; fabric laundry performance.
                                                                                                                                                                                                                                                                                                                                                RGIGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKSWGKWYVNTINIDGFRLDAVKH 238
                                                                                                                                                                                                                                                                                                                                                                          64 WKYQGEKEKKLYAVIDAFTQNNAFL--GVSDARYINALKLFLQGVTPLEYLAHRGFAHVG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      439
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                    21 RGLG--WETTYQPMDKVFPYDRYEGI-----KIHDWDKW------VDPFRLIMDAY 63
                                                               Detergent compositions for hard surface cleaning and laundry use contains Bacillus derived alpha amylase with improved thermostability, reduced calcium ion dependency etc.

Claim 1: Page 91: 97pp; English.

The present sequence is a Bacillus sp. alpha amylase with a specific activity at least 25% higher than that of Termamyl (RTM) at 25 to 55 degrees C at pH W to 10, measured by the Phadebas (RTM) machine dishwashing and laundry at a temperature of 10 to 25 degrees C. Improved cleaning, stain removal and fabric care are obtained by using it at a concentration of 0.00018 to 0.06%
                                                                                                                                                                                                                                                                                                                                                                                                                                 122 RHFTGEGARIACOMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 EDAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 TASKSGGTFDMRT------LMTNTLM------KDQPTL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 ---AVTFVDNHDIEPGGALQSWVDPWFKPLAYAFILTRQEGYPCVFYGDYYGIPQYNIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 LKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWIREGVIEKPGSGLAALIIDGPGGSKWMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 YAEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVP---T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   440 VGKQHAGKVFYDLT--GNR-----SDTVT----INSDGWGEF-KVNGGSV-SVWVPRKTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SWEM
                                                                                                                                                                                                                                                                                                                                                                                                        ----SFFPDWLSDVRSQTGKPLFTVG----EYWSY----
                                                                                                                                                                                                                                                                                              Indels 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of specific alpha-amylase enzymes - in laundry detergent
                                                                                                                                                                                                                                                                 3.6%; Score 104; DB 1; Length 515; 18.3%; Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      |::|:|:|:|:|:
----DINKLHNYIMKTN--GTMSLFDAPLHN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 GIECIKFLLEQDPDNVPIVQRWIDKWF--------WRGYRLL-
                                                                                                                                                                                                                                                                                             125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TLVA------MMMDYMQPKRVMSW-RE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PROC ) PROCTER & GAMBLE CO.
Baeck AC, Jones LA, Ohtani R, Pramod K, Rai S,
           (PROC ) PROCTER & GAMBLE CO.
Baeck AC, Jones LA, Ohtani R, Pramod K, Rai
Showell MS, Ward G;
                                                                                                                                                                                                                                                                                             43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 EDEMGWLSAKYP--DSFDRYKRPRFDHW 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        487 VSTIAWSITTRPWTDEFVRWTEPRLVAW 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W48263 standard; protein; 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                          82; Conservative
 07-MAR-1996; WO-U03276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1996; U12612.
01-AUG-1996; WO-U12612.
                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        239 IKF-----
                                                     WPI; 97-457524/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 98-159168/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-JUL-1998 (fi
Bacillus sp. alp
Alpha amylase; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus sp. WO9805748-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Showell MS;
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o,
                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                 179
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The sequence is that encoded by a homologue of the MLO gene, wild-type MLO exerts a negative regulatory function on a pathogen defence response, such that mutants exhibit a defence response in the absence of pathogen. Down-regulation or out-competition of MLO function may be used to
                                                                                                            which is
be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 RHFTGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFF 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 LKSKIDPLLIARRDYAYGTQHDYLDHSDIIGWTREGVTEKPGSGLAALIIDGPGGSKWWY 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 YAEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVP---T 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 VGKQHAGKVFYDLT--GNR----SDTVT----INSDGWGEF-KVNGGSV-SVWVPRKTT 486
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KIHDWDKW-----VDPFRLTMDAY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 RGIGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKSWGKWYVNTINIDGFRLDAVKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 WKYQGEKEKKLYAVIDAFIQNNAFL--GVSDARYINALKLFLQGVIPLEYLAHRGFAHVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated Mlo gene of barley - used to develop products for the production of transgenic plants which have increased pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 EDAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 ---AVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGYPCVFYGDYYGIPQYNIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   239 IKF-----EYWSY-----SPEPDWLSDVRSQTGKPLFTVG----EYWSY-----
compositions to provide effective cleaning and whitening of dingy
                                                                                                                                                                                                                                                                                                                                                                                                      Indels 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 TASKSGGTFDMRT-----LMTNTLM------KDQPTL-----
                                                             Claim 1; Page 74; 82pp; English.
This sequence represents an alpha amylase from Bacillus sp. vased in a laundry detergent. The detergent compositions can lfor boosting fabric laundry performance or for dingy fabric cleanup.
Sequence 515 AA;
                                                                                                                                                                                                                                                                                                                                     DB 1; Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---WRGYRLL-
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       269 ------DINKLHNYIMKTN--GTMSLFDAPLHN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----TLVA-----MMMDYMQPKRVMSW-RE-----
                                                                                                                                                                                                                                                                                                                                  Score 104; DB 1
Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INNE-) INNES CENT INNOVATIONS LTD JOHN.
Bueschiges R., Panstruga R, Schulzelefert PMJ;
WPI: 98-159149/14.
N-PSDB; V35031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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24;

SWEM 299 TDGPGGRKWMY 483 SAFHTWVPT 356 III	accharide; lactosidase.  aphlothermus, rom g, textile or -6GB4, deduced Thermotoga gh salt medium. 07-24) coding gy lucosidase, ty. Vectors and for producing es comprises fruit juice, maltose, maltose, werbascose, verbascose,	Length 684; Indels 197; Gaps 29;		
276TLVA	13 19873 standard; Protein; 684 AA. 19873 standard; Protein; 684 AA. 19873; 198 (first entry) 19973; 1998 (first entry) 1998 (sugar; baking; textile; detergent; beta-gale bermotoga maritima MSB8-6GB4; thermostable enzyme; oligosachermotoga maritima strain MSB8-6GB4. 19971 012623. 19971 012623. 19972 012623. 19973 012623. 19973 01299; 012-6939. 1998 (MS-949026. 19975 012-999; 012-6939. 1998 (MS-949026. 19975 012-999; 012-99	/ Match 3.4%; Score 98.5; DB 1; Local Similarity 18.3%; Pred. No. 0.17; nes 95; Conservative 67; Mismatches 159;		127 EGARIACQMQSIDELRHYQTETHAMSTYNKFPNGFHH 164 WGARIVTSGIWKPVYLEVYRARLQDSTAYLLELEGKDALVR-VNGFVHGEGNLIVEVYVN 164SNOWFDRVWYLSVPKSFFRDAYSSGPFEFTMAVSFSFFRFFWUTHILFV
QY Db Db QY Db	A W W W W W W W W W W W W W W W W W W W	Query Best Matc	Qy Db Qy Db	Oy Oy

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/note="derived from pre-ACE by removal of signal peptide"
223 GEKIGEFPVLEKNGEKLFDGVFHLKDVKLWY-----PWNVGKPYLYDFVFVLKDL--- 272
                                                                                                                     362
                                                                                                                                           317 IREPKG---WQD---AC-EGKDHI-----SHQAWSTFYGFNAASAFHTWVPTEDEMGW 362
                                                                                                                                                                                               363 LSAKYPDSFDRYYRPRFDHWGEQAR-----AGNRFYMKTLPMLC--QTCQIPMLFTEP- 413
                                                                                                                                                                                                                422 -------GFDEWGNMARKVDGINLGNRLYLFDFPELCAEEDPSTPYWPSSPY 466
                                     211 PFMSGAAYNGDMSIVIFGFSAQSDBSRHMTLGIECIKFLLEQDPDNVP-IVQRWIDKWFW 269
                                                      RGYRLLTLVAMMMDYMQPKRVMSW--RESWEMY-----AEQN----GGALFKDLARYG 316
                                                                                                                                                                     363 LCDELGIMVWQDFMYACLEYPDHLPWFRKLANEEARKIVRKLRYHPSIVLWC-GNNENNW 421
                                                                                                          W09003435-A.

2-ARR-1990.

27-SEP-1988; FR-012620.

27-SEP-1988; FR-012620.

(INRM) Institut National de la Sante et de la Recherche Medicale.
                                                                                                                                                                                                                                                                                                                                                            R04111;
07-SEP-1990 (first entry)
Human angiotensin converting enzyme (ACE)
human angiotensin converting enzyme; hypertension; bradykinin.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label_putative N-glycosylation site 523. 525 / label=putative N-glycosylation site 677. 679 / label=putative N-glycosylation site 713. 715 / label=putative N-glycosylation site / label=putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160. .162
/label-putative N-glycosylation site
318. .320
/label-putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74. 76
/label=putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145. .447
| Tabel=putative N-glycosylation site
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/label=putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label=putative N-glycosylation site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4. .56
Tabel=putative N-glycosylation site
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// Abel=putative N-glycosylation site
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/label=putative N-glycosylation site
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/label=putative N-glycosylation
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/label=putative N-glycosylation
                                                                                                                                                                                                                                                    414 ----GNPTKIGARE-----SNYLGNKFHFCSD 436
                                                                                                                                                                                                                                                                       467 GGEKANSEKEGDRHVWYVWSGWMNYENYEKNTGRFISE 504
                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 30. .1277
                                                                                                                                                                                                                                                                                                                                                                                                                                             30. .1277
/label-mature ACE
                                                                                                                                                                                                                                                                                                                                               R04111 standard; peptide; 1306 AA.
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46;
                                                                        Human angiotensin converting enzyme hydrolyses angiotensin I and kinins. Either intext enzyme or fragments thereof can be used to generate antibodies for diagnostic use. Oligonucleotide probes can also be made which are complementary to the sequence encoding the enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             979 NLEDLVVAHHEMGHIQYFMQYKDLPVALREGANP---GFHEAIGDVLALSVSTPKHLHSL 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1036 NILSSEGGSDEHDINFLMKMALDKIAFIPFSYLVDQWRWRVFDGSITKENYNQEWWSLRL 1095
                                                                                                                                                                                                                                                                                                                                                                                                         226
                                                                                                                                                                                                                                                                                                                                                                                                                                                          244
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                                                                                                                                                                                                                                                                                                                                                                                                                                 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        811 QAARLNGYVDAGDSWRSMYETPSLEQDLERLFQELQPLYLNLHAYVRRALHRHYGAQ--- 867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----HINLEGPIPAHLLGNMWAQTWSNIYDLVVPFPSAPSMDT---TEAMLKQGWTPRRM 920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----FHFCSDHCK-DIFDHE--PQKYVQAWLPVHQ 458
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                  428 VSTPEHLHKIGLLDR---VTNDTESDINYLLKMALEKIAFLPF----GYLVDQW-RWGVF 479
                                                                                                                                                                                                                                                          ---VDPFRLTMDAYW----KYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQG 105
                                                                                                                                                                                                                                                                                  SGRTPPSRXNFD-WWYLRTKYQG-----ICPPVTRN-----ETHFDAGAKFHVPN 523
                                                                                                                                                                                                                                                                                                                                  524 VIPYIRYFVSFVLQFQFHEALCKEAGYEGPLHQCDIYRSTKAGAKLRKVLQAGSSRPWQE 583
                                                                                                                                                                                                                                                                                                                                                          -----SIDE---LRHYQIETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFEDA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NHTLKYGTQARKFDVNQLQNTTIKRIIKKVQDLERAALPAQELEEYNKILLDMETTYSVA 754
                                                                                                                                                                                                                                                                                                                                                                                                                                YPEG-IDLVTDEAEASKFVEEYDRTSQVVWNEYAEANWNYNTNITTETSKILLQKNMQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -SWRESWEMYA-EQNGGALFKDL------ARYGIREPKGWQDAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------HQAWSTFYG----FNAASAFHTWVPTED--EMGWLSAKY
                                                                                                                                                                                                                                                                                                                                                                                  584 VLKDMVGLDALDAQPLLKYFQPVTQWLQEQNQ-QNG--EVLGWPEYQWHPPLP----DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -DESRHMTLGIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CIKFLLEQDPDNVPIVQRWIDK--WFWRGYRLLTLVAMMMDYMQPKRVM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              921 FKEADDFFTSLGLLPVPPEF--WNKSMLEKPTDGREVVCHASAWDFYNGKDFRIKOCTTV
                                   New DNA encoding human angiotensin converting enzyme used eg in diagnosis of hypertension, evaluation of enzyme inhibitors Disclosure; p; French.
                                                                                                                                                                       ; Pred. No. 1.2;
80; Mismatches 214; Indels 321;
                                                                                                                                                                                                            1 MDTPILKKKLGLKDRYAAMTRGLGWETTY ---QPMDKV--FPYDRYEGIKIHDWDKW-
                                                                                                                                                              DB 1; Length 1306;
                                                                                                                                                                                                                                                                                                           VTP------LEYLAHRGFAHVGRH------FTGEGARIACQMQ--
                                                                                                                                                                                                                                                                                                                                                                                                          YSSGPFEFLT ----AVSFSFEYVLTNLLFVPFMSGA--AYNGDMSTVT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 PDSFDRYR-----PRFDHWG----EQARAGNR-----FY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -MKTLPMLCQTCQIPMLFTEPGNPTKIGARES--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alhenc-Gelas F, Hubert C, Corvol P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IHOGNCFPP-----DADPGAEGFDPLAAVLDYYAVT 489
                                                                                                                                                             3.3%; Score 94.5; 18.8%; Pred. No. 1.
                                                                                                                                                           Query Match 3.39
Best Local Similarity 18.89
Matches 142; Conservative
                                                                                                                        1306 AA;
Soubrier F, Alhenc WPI; 90-132272/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----FGESAQS-
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                                                                                                                           Sequence
                          N-PSDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 695
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                                                                                                                                                                                                                                                                                  480
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W69165 standard; Protein; 1965 AA.

RESULT 15 W69165

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protein, and comparing IAA protease activity in the presence and absence of a test compound. S. pneumoniae cells or isolated IBAA protease enzyme can be used in this method. The antibiotic is used to treat S. pneumoniae or other bacterial infections. The invention also relates to a subunit vaccine comprising an isolated the severity of (S. pneumoniae) infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA encoding Streptococcus pneumoniae IgA protease - and antibiotic screening assay and subunit vaccine etc claim 11; Fig 4; 66pp; English.

This is the amino acid sequence of Streptococcus pneumoniae IgA protease, deduced from an isolated iga gene (see V69165). The invention provides a method of identifying a candidate antibiotic compound that involves incubating the IgA protease with an IgA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1605. .1609
/note= "zinc binding domain (with residue 1629)"
                                                                                                                                                                                                                                                                                               "hydrophilic region comprising multiple tandem repeats"
                                                                                                          anchor for
                                                                                                      /note= "region resembles C-terminal anchor for other Gram-positive surface proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "zinc binding domain (with residues 1605-1609)"
                                     antibiotic; vaccine
                                                                                                                                                                                                                              "lysine-rich charged region"
                                                                                                                                                                                                                                                                "ATP/GTP binding consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-1996; US-026939.
(CHIL.) CHILDRENS HOSPITAL PHILADELPHIA.
(PRET.) NEW ENGLAND MEDICAL CENT HOSPITALS INC.
Gilbert-Rothstein JV, Plaut AG, Weiser JN;
                                                                                                                                                                                          'note= "hydrophobic region"
07-DEC-1998 (first entry)
Streptococcus pneumoniae IgA protease.
IgA protease; meningitis; pneumonia; a:
Streptococcus pneumoniae strain P110.
Location/Qualifiers
                                                                                                                                                         /note= "LPNTGS motif"
102. .125
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187. .19
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472. ..4
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31-JAN-1997; 196502.
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N-PSDB; V44592.
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                                                                                                                                                                74 LYAVIDA--FTQNNAFLGVSDARYINALKIFLQGVTPLE------YLAHRG 116
                                                                                                                                                                                                                                                  117 FAHVGR------PFTGEGARIACQMQSID----ELRHYQTETHAMST---YNKFFNGF 161
                                                                                                                                                                                                                                                                                                                                 162 HHSNQWF--DRVWYLSVPKSFFEDA-----YSSGPFEFLTAVSFSFEYVLTNLLF 209
                                                                                                                                                                                                                                                                                                                                                                                                               210 VPFMSGAAYNGDMSTVTFGFSAQSDESRAMTLGIECIKFLLEQDPDNVPIVQRWIDKWFW 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 RGYRLLTLVAMMMDYMQPKRVMSWRESWEMYAEQNGGALFKDLARYGIREPKGWQDACEG 329
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Query Match 3.3%; Score 94; DB 1; Length 1965; Best Local Similarity 21.0%; Pred. No. 2.4; Matches 97; Conservative 56; Mismatches 193; Indels 116; Gaps
                                                                                  36 FPYDRYEGIK-----GEKEKK 73
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Search completed: September 26, 2000, 20:11:49 Job time: 10373 sec

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us-09-430-029-5.rai

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

September 26, 2000, 20:22:40; Search time 60.65 Seconds (without alignments) 130.418 Million cell updates/sec Run on:

US-09-430-029-5 Title:

2873 Perfect score:

1 MDTPTLKKKLGLKDRYAAMT.......FDGSEDQKNFAAWRGQATRN 516 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

152396 seqs, 15329161 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 4, Appli		. ~	25,	10,	517	2,	37,	Ŋ	m	35,	37	9	9	35,	m	2.7	'n	80	33,	3	é	è	è	9	ω.	6, Appl	Patent No. 5256558
SUMMARIES	ID	US-08-319-387-4	5171684-2	08 - 499	-917-299-2	08 - 917		-466-	-08-468-700	-645-971-	-468-220-3	US-08-468-698-35	-704	US-08-890-383-6	US-08-914-679A-6	PCT-US94-01553A-35	PCT-US95-10426-35	US-09-095-163-2	US-08-176-414B-3	US-08-477-451-8	3-162	-780-872	3-720-899	US-08-459-610-6	-804	US-08-687-399-6	US-08-600-908A-6	0	5256558-4
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	Score	2409	374.5	370	255	192	152	109	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5	91.5	90.5	06	90	88	68	88	88	88	88	88	88	88
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Sequence 4, Appli	Sequence 2, Appli	Sequence 24, Appl	Sequence 13, Appl	Sequence 13, Appl	Sequence 4, Appli	Sequence 7, Appli	Sequence 17, Appl	26.	Sequence 1, Appli	Patent No. 5217865	Sequence 6, Appli	, ,	α		Sequence 21, Appl
US-08-849-212-4 US-08-785-071A-2	US-09-012-872-2	US-08-335-844A-24	US-08-272-255-13	PCT-US95-08565-13	PCT-US96-12860-4	US-08-833-610-7	US-08-834-033A-17	US-08-917-299-26	US-08-750-141A-1	5217865-2	US-08-511-485-6	US-08-386-727-8	US-08-600-452A-8	PCT-US95-05922A-2	US-08-392-625-21
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713	876	972	475	4/5	604	365	365	52	916	529	604	998	866	438	455
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88	87	86.5	0. U. U.	90.0	84.5	80.5	80.5	80	80	79.5	79.5	79	79	78.5	78.5
30	31	32	3. C.	<b>5</b> €	35	36	37	38	39	40	41	42	43	44	45

#### ALIGNMENTS

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Sequence 4, Application US/08319387
Patent No. 554317
Patent No. 554317
GENERAL INFORMATION:
APPLICANT: Shields, Malcolm S.
APPLICANT: Francesconi, Stephen C.
TITLE OF INVENTION: Microbial Degradation of Trichloroethylene, TITLE OF INVENTION: Dichloroethylenes and Aromatic Pollutants NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS: ADDRESSEE: Saliwanchik & Saliwanchik
                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DAIR:
APPLICATION NUMBER: US/08/319,387
                                                                                                                                                                                                            ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/167,457
FILING DATE: 15-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 07/694,718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION: 15-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36 965
REFERENCE/DOCKET NUMBER: UN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 02-MAY-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 519 amino acids TYPE: amino acid STRANDEDNESS: single
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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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US-08-319-387-4
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NMATFGMMDELRHGQLQLFFPHEYCKKDRQFDWAWRAYHSNE-----WAAIAAKHFFDDI 179
                                                                                                                                                                         301 AEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQ-----AWSTFYGFNAASAFHTWV 354
                                                                                                                                                                                                                                            355 PTEDEMGWLSAKYPDSFDRYYRPRFDHWGE------QARAGNRFYM---KTLPMLCQTCQ 405
                                                      -TPEERDWLEEKYPGWNKR------WGRCWDVITENVLNDRMDLVSPETLPSVCNMSQ
                                                                                                                                                                                                                                                                                                               406 IPMLETEPGNPTKIGARESNYLGNKFHFCSDHCKDIFDHEPQKYVQAWLPVHQIHQGNCF
                                                                                                     ECIKFLLEQDPDNVPIVQRWIDKWFWRGYRLL-TLVAMMMDYMQP--KRVMSWRESWEMY
                                                                                                                                                                                                        296 -EWIIGQFERSLIDLGLDKPWYWDLFLKDIDELHHSYHMGVLDWRTTAWWNPAAGV----
                                  185 YSS-GPFEFLTAVSFSFEYVLTHLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGI
                                                                                                                                                                                                                                                                                                                                                                                      466 PPDADPGAE--GFDPLAAVLDYYAVTMGRDNLDF
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APPLICATION WUMBER: JP Hei-6-179689
FILING DATE: 08-JUL-1994
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Ve
& WordPerfect version 5.1
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Patent No. 5612204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COmpatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sughrue, Mion, STREET: 2100 Pennsylvania
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25.6%;
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Saeki, Hisashi
APPLICANT: Miura, Akira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 501 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-499-215-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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20037-3202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
US-08-499-215-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAGAYSVKAALERAKIYEN-SDPGWISTLKSHYGAIAVGETAAVTGEGRMARFSKAPGNR 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 IACQMQSIDELRHYQTETHAMSTYNKFFNGF-----HHSNQWFDRVWYLSVPKSFFEDA 184
                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                        GRHFTGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSF 180
                                                                                                                                                                                                                                                                                                                                                                                                                         AEQNGGALFKDLARYGIREPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEM 360
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                                                                                                                                          61 DAYWKYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHV 120
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                                                                                         1 MDTPTLKKKLGLKDRYAAMTRGLGWETTYQPMDKVFPYDRYEGIKIHDWDKWVDFFRLTM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 KDWY-ELTRATNWTPSYVTEEQLFPERMSGHMGIPLEKWESYDEPYKTSYPEYVSIQREK
                                                                                                                                                                                                                               FEDAYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSCAAYNGDMSTVTFGFSAQSDESRHMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YEN, KWANG-MU; BLATT, LAWRENCE M.; KARL, MICHAEL R.
TITLE OF INVENTION: BIOCONVERSIONS CATALYZED BY THE TOULUENE
MONOXYGEARSE OF PSEUDOMANAS MENDOCINA KR-1
NUMBER OF SEQUENCES: 41
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/590,374
FILING DATE: 28-SEP-1990
PRIOR APPLICATION AND ATA:
APPLICATION NUMBER: 177,631
FILING DATE: 05-APR-1988
   Length 519;
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; Pred. No. 2.5e-33;
71; Mismatches 244;
83.8%; Score 2409; DB 1;
81.8%; Pred. No. 1.2e-261;
ive 48; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVLDYYAVTMGRDNLDFDGSEDQKNFAAWRGQ 512
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26.5%;
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                                      Conservative
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                     Similarity
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;Patent No. 5171684
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                                    Matches 419;
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Best Local S:
Matches 136,
   Query Match
Best Local 9
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TITLE OF INVENTION: BIOLOGICAL DEGRADATIVE
TITLE OF INVENTION: TREATMENT OF CHLORINE-SUBSTITUTED ETHYLENE
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 501;
                                                                                                                                                                                                                                                                                  Version #1.30
                                                                               Zinn, Macpeak & Seas
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52 amino acids

LENGIH:

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240 ILGIECIKFILEQDPDNVPIVQRWIDKWFWRGYRLL-TLVAMMMDYMQPKRVMSWRESWE 298
79 DAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGRHFTGEGARIACQMQSI 138
                                                                                                            124 DEVRHAQLE---MILRN-----YYAKHWCD------PSGFDIGQRGIYQHPAGLVSIG 167
                                                                                                                                                               239
                                                                                                                                                                                 299 MYAEQN--GGALFKDLARYGIREPKGWQDACEG-----KDHISHQAWSTFYGFNAAS 348
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287 EWVVDDFVGGYIDR-LSEFGVQAP-----ACLGAAADEVKWSHHTLGGVLSAVWPLN--- 337
                                                                                                                                                                                                                                                                                                                                                                                         349 AFHTWVPTEDEMG----WLSAKYPDSFDRYYRPRFDHW-GEQA---RAGNRFYMKTLPM 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---FW--RSDAMGPADFEWFENHYPGWSAAYQ----GYWEGYKALADPAGGRIMLQELPG 388
                                                                                                                                                       181 -FEDAYSSGPFEFLTAVSFSFEYVLFNLLFVPFMSGAAYNGDMSTVTFGFSAQSDESRHM
                                                                                                                                                                                                                                                         400 L---CQTCQIPMLFTEPGNPTKIGARESNYLGNKFHFCSDHCKDIFDHEPQKY---VQAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25, Application US/08917299
Patent No. 6010855
GENERAL INFORMATION
APPLICANT: JACKSON, MARY
APPLICANT: GLQUEL, Brigitte
TILLE OF INVENTION: DESATURASE ANTIGEN OF MYCOBACTERIUM
TILLE OF INVENTION: TUBERCULOSIS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c/o Finnegan Henderson, Farrabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.30
                                                                         139 DELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0156-00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/022,713
FILING DATE: 26-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/917,299 FILING DATE: 25-JUL-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Dunner, L.L.P
STREET: 1300 I Street, N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.9%; Score 255; DB 3; Length 52; Best Local Similarity 94.2%; Pred. No. 1.7e-21; Matches 49; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                               Length 52;
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: JACKSON, MARY
APPLICANT: GIQUEL, Brigitte
TITLE OF INVENTION: DESAURASE ANTIGEN OF MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
NUMBER OF SQUENCES: 37
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: c/o Finnegan Henderson, Farrabow, Garrett ADDRESSEE: Dunner, L.L.P
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/917,299
FILING DATE: 25-UL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.7%; Score 192; DB 3; 70.6%; Pred. No. 2e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 03495.0156-00 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       us 60/022,713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                               US-08-917-299-10
Sequence 10, Application US/08917299
Patent No. 6010855
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MEYERS, Kenneth J. REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEO ID NO: 10.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 26-JUL-1996
ATTORNEY/AGENT INFORMATION:
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                    single
                                                   peptide
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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COMPUTER READABLE FORM:
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TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: pept:
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Matches 36; Conserv
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                                                                  US-08-917-299-25
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                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 QNNAFLGVSDARYINALKLFLQGVTPLEYLAH---RGFAHVGRHFTGEGARIACQMQSID 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 EREHDQMVREGWEHTMARCY----SPLRYLFHCLQMSSAYVQQMAPASTISNCCILQTAD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 VSFSFEYVLTNL------LFVPFMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIECI 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43 WELSPDSPMNLWYKQYRNASPLKHDNWDAFTDPDQLVYRTYNLMQDGQESYVQSLFDQFN 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 WE-TTYQPMDKVF-PYDRYEGIKIHDWDKWVDPFRLTMDAYWKYQGEKEKKLYAVIDAFT 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Saeki, Hisashi
APPLICANT: Miura, Akira
TITLE OF INVENTION: BIOLOGICAL DEGRADATIVE
TITLE OF INVENTION: TREATMENT OF CHLORINE-SUBSTITUTED ETHYLENE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                           APPLICANT: YEN, KWANG-MU; BLATT, LAWRENCE M.; KARL, MICHAEL R. TITLE OF INVENTION: BIOCONVERSIONS CATALYZED BY THE TOULUENE; MONOXYGENASE OF PSEUDOMAAS MENDOCINA KR-1 NUMBER OF SEQUENCES: 41 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                               Length 327;
                                                                                                                                                                                                                                                                                                                                                                               5.3%; Score 152; DB 5; Length 32 24.5%; Pred. No. 1.2e-08; tive 34; Mismatches 131; Indels
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08-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Ve
SOFTWARE: & WordPerfect version 5...
CURRENT APPLICATION DATA:
                                                                                                                                                       APPLICATION NUMBER: US/07/590,374
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 177,631
FILING DATE: 05-APR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/499,215
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER:
FILING DATE: 08-JUL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 64; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Washingto
COUNTRY: U.S.A.
ZIP: 20037-3202
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5171684-6; Patent No. 5171684
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                                                                                                                                                                                                                                                                                               LENGTH: 327
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NLLFVP-FMSGAAYNGDMSTVTFGFSAQSDESRHMTLGIECIKFLLEQDP----DNVPIV 260
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                                                                                                                                                                                                                                                                                                                                -EYLAHRGFAHVGRHFTGEGARIACQMQSIDELRHYQTE 147
                                                                                                                                                                                                                                                                                                                                                                                                             148 THAMSTYNKF--FNGFHHSNQWFDRVWYLSVPKSFFEDAYSSGPFEFLTAVSFSFEYVLT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 VHHLDHLQESPEFSDAGAREAWMSDSTLVPIREVIERIAASQDWVEILVAGTLVFEPLVG
                                                                                                                                                              3.8%; Score 109; DB 1; Length 342; 19.4%; Pred. No. 0.00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/468,700
FILING DATE: 06-UUN-1995
                                                                                                                                                                                                                                                                            68 VRISEWSAYRDPHQLWQRPYVSTCNQDQQALARLVPVLTMGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37, Application US/08468700
Patent No. 5736499
GENERAL INFORMATION:
APPLICANT: COLIN MITCHINSON
APPLICANT: CAROL A. REGUADT
APPLICANT: TRACI H. ROPP
APPLICANT: TEIF P. SOTHEIM
ITTE OF INVENTION: WUTANT ALPHA-AMYLASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: US/08/468,700
06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                       39;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            South San Francisco
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ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  548 amino acids
                     342 amino acids
                                                                                                                                                                                                         Conservative
SEQUENCE CHARACTERISTICS
                                                                             ; MOLECULE TYPE: protein US-08-499-215-2
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COMPUTER READABLE FORM:
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                                        amino acid
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Matches 48; Conserv
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289 RRWIEEW 295
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US-08-468-700-37
                                                            TOPOLOGY:
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                       LENGTH:
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64 WKYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGRH 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWL----SAKYPDSFD 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R----SDTVT----INSDGWGEF-KVNGGSV-SVWVPRKTTVSTIARPITTRPWTGEFV 537
                                                                                                                                                                                                                                                                                            333 SKSGGAFDMRT-----LMTNTLM------KDQPTLAVTFVDNHDTNPAKRCSH 374
                                                                                                                                      268 ---DGLKHIKFSFFPD------WLSYVRSQTGKPLFTVG----EYWSY-----
                                                                                                                                                                                                                                                       184 AYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMST--VTFGFSAQSDESRHMTL
                                                                                                                                                                                                                                                                                                                                     -----NVPIVQRWIDKWF--WRGYRLLTLVA
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APPLICANT: Power, Scott D.
APPLICANT: Power, Scott D.
APPLICANT: Solheim, Leif P.
TILE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Generor.
                                                                                                                                                                                                                    --------DINKLHNYITKTN--GTMSLFDAPLHN----
                                    - KIHDWDKW-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,220 FILING DATE: 06-UNN-95
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35, Application US/08468220
Patent No. 5824532
GENERAL INFORMATION:
APPLICANT: Antrim, Richard L.
APPLICANT: Barnett, Christopher
APPLICANT: Mitchinson, Colin
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FILING DATE: 10-FEB-94
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                               21 RGLG--WETTYQPMDKVFPYDRYEGI-
                                                                                                                                                                                                                                                                                                                                 242 GIECIK----FLLEQUPD----
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ATTORNEY/AGENT INFORMATION:
NAME: Stone, Christopher L.
REGISTRATION NUMBER: 35.696
REFERENCE/DOCKET NUMBER: 696
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APPLICATION NUMBER: (
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                                                                                                                                                                                                      213 RGIGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRL---- 267
                                                                                                                                                                                                                                                                                                                   124 FTGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFED 183
                                                                                                                                                                                                                                                                                                                                                                                                                              SKSGGAFDMRT-----LMTNTLM------KDQPTLAVTFVDNHDTNPAKRCSH 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 REPRGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWL----SAKYPDSFD 372
                                                                                                                                                                                                                                                                                                                                                                  -----KFYTA 332
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                                                                                                                                                                         -----VDPFRLTMDAY 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NVPIVQRWIDKWF--WRGYRLLTLVA
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                                                                                                                                      Indels 163;
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                                                                                                 Length 548;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
TITLE OF INVENTION: Modified Alpha-Amylases Having Altered
TITLE OF INVENTION: Calcium Binding Properties
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                        -----DINKLHNYITKTN--GTMSLFDAPLHN-----
                                                                                                                                49; Mismatches 136;
                                                                                                                                                                   21 RGLG--WETTYQPMDKVFPYDRYEGI------KIHDWDKW-
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                                                                                                 DB 1;
                                                                                               Score 91.5; DB
Pred. No. 0.16;
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Patent No. 5763385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WUMBER OF SEQUENCES: 5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                         Query Match 3.2%;
Best Local Similarity 19.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 GIECIK----FLLEQDPD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 MMMDYMQPKRVMSW-----
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                                                                                                                                82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
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; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-468-700-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:: || | |
538 RWHEPRLVAW 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM:
US-08-645-971-5
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                                                                                                                              Matches
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303 -----DINKLHNYITKTN--GTMSLFDAPLHN---
                Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.2%; Score 91.5; DB 2; 19.1%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENENCOR INTERNATIONAL, INC. COLIN MITCHINSON
                                                                                                                                                                                                                                              NAME: Scone, Christopher L.
REGISTRATION NUMBER: 35,696
REFERENCE/POCKET NUMBER: GC220D2
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 742-7555
TELEFAX: (415) 742-7551
INFORMATION FOR SEQ ID NO: 35:
                                                  APPLICATION NUMBER: US/08/468,690
CLASSIFICATION: 435
PRIOR APPLICATION DATE: 06-UNA-95
PRIOR APPLICATION DATE: 08/194,664
FILING DATE: 10-FEB-94
PRIOR APPLICATION DATE: 08/106,395
FILING DATE: 11-FEB-93
ATTORNEY/AGRIT IR-FEB-93
ATTORNEY/AGRIT IR-FEB-93
ATTORNEY/AGRIT IR-FEB-93
ATTORNEY/AGRIT IR-FEB-93
ATTORNEY/AGRIT IR-FEB-93
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3.08-104-706A-37

Sequence 37, Application US/08704706A

Patent No. 5958739

GENERAL INFORMATION:
APPLICANT: GENEROCA INTERNATIONAL
APPLICANT: COLIN MITCHINSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 RGLG--WETTYQPMDKVFPYDRYEGI----
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acids
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                  SOFTWARE: Patentin Rel. CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 82; Conserva
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|538 RWHEPRLVAW 547
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                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                               302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----RESWEMYAEQNGGALFKDLARYGI.317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FTGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFFED 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------DINKLHNYITKTN--GTMSLFDAPLHN-------KFYTA 332
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                                                                                                                                                                                                                                                                                                                                                                     213 RGIGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRL----
                                                                                                                                                                                                                                                                                          Indels 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                               ---DGLKHIKESFFPD------WLSYVRSQTGKPLFTVG----EYWSY----
                                                                                                                                                                                                                                                      Length 548;
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                                                                                                                                                                                                                                                    3.2%; Score 91.5; DB 2; I
19.1%; Pred. No. 0.16;
ive 49; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                  -KIHDWDKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35, Application US/08468698 Patent No. 5849549
                                                                                                                                                                                                                                                                                                                                  21 RGLG--WETTYQPMDKVFPYDRYEGI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Antrim, Richard L.
APPLICANT: Barnett, Christopher
APPLICANT: Mitchinson, Colin
APPLICANT: Power, Scott D.
APPLICANT: Requadt, Carol
APPLICANT: Solheim, Leif P.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 742-7555
TELEPAX: (415) 742-7217
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 180 Kimball Way
South San Francisco
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Matches 82; Conservative
                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-468-220-35
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                                                                                                                  amino acid
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64 WKYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGRH 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 AYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMST--VTFGFSAQSDESRHMTL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 SKSGGAFDMRT-----LMTNTLM-----KDQPTLAVTFVDNHDTNPAKRCSH 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---NVPIVQRWIDKWF--WRGYRLLILVA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             432 -QHDYLDHSDIIGWTREGVTEKPGSGLAALITDGAGRSKWMYVGKQHAGKVFYDLT--GN 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 REPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWL-----SAKYPDSFD 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  489 R----SDTVT----INSDGWGEF-KVNGGSV-SVWVPRKTIVSTIARPITTRPWTGEFV 537
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                 268 ----DGLKHIKFSFFPD------WLSYVRSQTGKPLFTVG----EYWSY-----
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                                                                                                                                                                                                           213 RGIGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRL----
                                                              Indels 163;
Length 548;
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213 RGIGKAWDWEVDIENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRL---- 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 WKYQGEKEKKLYAVIDAFTQNNAFLGVSDARYINALKLFLQGVTPLEYLAHRGFAHVGRH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 -------PINKLHNYITKIN--GTMSLFDAPLHN-------KFYTA 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 GIECIK-----FLLEQDPD------NVPIVQRWIDKWF--WRGYRLLTLVA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 REPKGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWL----SAKYPDSFD 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 GRPWFKPLAYAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGT--- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RESWEMYAEQNGGALFKDLARYGI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 -QHDYLDHSDIIGWTREGVTEKPGSGLAALITDGAGRSKWMYVGKQHAGKVFYDLT--GN 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | : : : : | 489 R----SDTVT----INSDGWGEF-KVNGGSV-SVWVPRKTTVSTIARPITTRPWTGEFV 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 SKSGGAFDMRT-----LMTNTLM------KDQPTLAVTFVDNHDTNPAKRCSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 163;
                                                                                                                     APPLICANT: Anthony G. Day
TITLE OF INVENTION: MTANT ALPHA-AMYLASE HAVING INTRODUCED
TITLE OF INVENTION: THEREIN A DISULFIDE BOND
WOUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---DGLKHIKFSFFPD-----WLSYVRSQTGKPLFTVG----EYWSY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.2%; Score 91.5; DB 3;
19.1%; Pred. No. 0.16;
ive 49; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---KIHDWDKW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/080,383
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                           SEE: Genencor International, Inc.: 925 Page Mill Road
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 RGLG--WETTYQPMDKVFPYDRYEGI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: GC377
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 846-7555
                                                         Sequence 6, Application US/08890383 Patent No. 6008026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (650) 846-7555
TELEFAX: (650) 845-6504
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Stone, Christopher REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 548 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: protein US-08~890-383-6
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                                                                                                       GENERAL INFORMATION:
APPLICANT: Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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Best Local Similarity
Matches 82; Conserva
                                                                                                                                                                                                                                                                                                                                   Y: USA
94304-1013
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                                                                                                                                                                                                                                           ADDRESSEE:
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                                  US-08-890-383-6
                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 FTGEGARIACQMQSIDELRHYQTETHAMSTYNKFFNGFHHSNQWFDRVWYLSVPKSFPED 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 SKSGGAFDMRT-----LMINTLM------KDQPTLAVTFVDNHDTNPAKRCSH 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----NVPIVQRWIDKWF--WRGYRLLTLVA 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 GRPWFKPLAYAPILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGT--- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11: 1: 1 | 1 | 1 | 1 | 432 -QHDYLDHSDIIGWTREGVTEKPGSGLAALITDGAGRSKWMYVGKQHAGKVFYDLT--GN 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 REPRGWQDACEGKDHISHQAWSTFYGFNAASAFHTWVPTEDEMGWL----SAKYPDSFD 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESWEMYAEQNGGALFKDLARYGI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489 R----SDIVT----INSDGWGEF-KVNGGSV-SVWVPRKTIVSTIARPITIRPWIGEFV 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 RGLG--WETTYQPMDKVFPYDRYEGI------KIHDWDKW------VDPFRLTMDAY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              268 ---DGLKHIKFSFFPD-----WLSYVRSQTGKPLFTVG----EYWSY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213 RGIGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTINIDGFRL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49; Mismatches 136; Indels 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.2%; Score 91.5; DB 2; Length 548; 19.1%; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,706A
                                                                                          ADDRESSEE: Genencor International, Inc. STREET: 925 Page Mill Road
APPLICANT: ANDREW SHAW
TITLE OF INVENTYON: MUTANT ALPHA-AMYLASE
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
DATE OF THE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: FEBRUARY 20, 1998
CLASSIFICATION: 435
ATTORNEY/AGENI INFORMATION:
NAME: Stone, Christopher
REGISTRATION NUMBER: 35,696
REFERENCE/DOCKET NUMBER: GC275
TELECOMUNICATION INFORMATION:
TELEPRONE: (650) 846-755
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      February 20, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: unknown; MOLECULE TYPE: protein US-08-704-706A-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 MMMDYMQPKRVMSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      538 RWHEPRLVAW 547
                                                                                                                                     Palo Alto
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                                                                                                                                                                                    USA
                                                                                                                                                          STATE: C
COUNTRY:
                                                                                                              STREET:
CITY: Pa
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AYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMST--VTFGFSAQSDESRHMTL 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- KFYTA 332
                                    432 -QHDYLDHSDIIGWTREGVTEKPGSGLAALITDGAGRSKWMYVGKQHAGKVFYDLT--GN 488
                                                                               REPKGWQDACEGKDHISHQAWSTFYGFNAASAFHIWVPTEDEMGWL-----SAKYPDSFD 372
                                                                                                             R----SDIVI----INSDGWGEF-KVNGGSV-SVWVPRKTIVSIIARPITIRPWIGEFV 537
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-RESWEMYAEONGGALFKDLARYGI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          213 RGIGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKNWGKWYVNTTNIDGFRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 3.2%; Score 91.5; DB 4; Length 548; Best Local Similarity 19.1%; Pred. No. 0.16; Matches 82; Conservative 49; Mismatches 136; Indels 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---DGLKHIKFSFFPD-----BLSYVRSQTGKPLFTVG----EYWSY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---DINKLHNYITKTN--GTMSLFDAPLHN------
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GENENCOR INTERNTIONAL, INC.
TITLE OF INVENTION: Oxidatively Stable Alpha-Amylase
NUMBER OF SEQUENCES: 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US94/01553A
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                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 180 Kimball Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                         Sequence 35, Application PC/TUS9401553A GENERAL INFORMATION:
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NAME: HOTN, MARGATER A.
REGISTRATION NUMBER: 33,401
REFERENCE/DOCKET NUMBER: GC22(
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 742-7536
TELEPHONE: (415) 742-7217
INFORMATION FOR SFO ID NO: 35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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amino acid
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; MOLECULE TYPE: protein
PCT-US94-01553A-35
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    280 MMMDYMQPKRVMSW
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                                                                                                                                                                 373 RYYRPRFDHW 382
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                                                                                                                                                                                                                                                                        RESULT 15
PCT-US94-01553A-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 FTGEGARIACOMOSIDELRHYQIETHAMSTYNKFFNGFHHSNOWFDRVWYLSVPKSFFED 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------DINKLHNYITKTN--GTMSLFDAPLHN------KFYTA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 AYSSGPFEFLTAVSFSFEYVLTNLLFVPFMSGAAYNGDMST--VTFGFSAQSDESRHMTL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KDQPTLAVTFVDNHDTNPAKRCSH 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GRPWFKPLAYAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGT--- 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                      MUTANT ALPHA-AMYLASE COMPRISING MODIFICATION AT RESIDUES CORRESPONDING TO A210, H405 AND/OR T412 IN BACILLUS LICHENIFORMIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---DGLKHIKFSFFPD-----WLSYVRSQTGKPLFTVG----EYWSY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ore 91.5; DB 3;
ed. No. 0.16;
Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 RGLG--WEITYQPMDKVFPYDRYEGI------KIHDWDKW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION NUMBER: US/08/914,679A APPLIANG DAIE: TO Be Assigned
                                                                                                                                                                                                                                                                                                                                                                       E: Genencor International, Inc.
925 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.2%; Score 91.5; 19.1%; Pred. No. 0.
                                                                                                                                                                 Sequence 6, Application US/08914679A Patent No. 6080568 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: GC387
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----
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                                                                                                                                                                                                                                                       Swanson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stone, Christopher REGISTRATION NUMBER: 35,696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (650) 846-7555
TELEFAX: (650) 845-6504
INFORMATION FOR SEQ ID No: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: TO BE ASSIGNATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0uery Match
Best Local Similarity 19.1%
Matches 82; Conservative
                                                                                                                                                                                                                                APPLICANT: Anthony G. Day APPLICANT: Barbara A. Swa:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           548 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                      TITLE OF INVENTION: MITTLE OF INVENTION: AITLE OF INVENTION: TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                         373 RYYRPRFDHW 382
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Search completed: September 26, 2000, 20:22:44 Job time: 3818 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

September 26, 2000, 20:11:49; Search time 75.19 Seconds (without alignments) 37.172 Million cell updates/sec

US-09-430-029-6 666 Title: Perfect score:

1 MAVIALKPYDFPVKDAVEKF.....HKDLISFRTPGLDGLGGASF 118 Sednence:

Scoring table:

188963 seqs, 23686106 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Fragment of human Glucocorticoid ind	EGF-like homologue Amino acid sequenc	Eupenicillium bref Porcine retrovirus	Arabidopsis blue 1 Murine IL-4 recept	Murine interleukin Mouse interleukin	Mouse interleukin- Mouse interleukin-
W78326 W76426	Y05284 Y13346	W13405 W32091	R92/01 R11255 W13/09	W48313	W73471
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#### ALIGNMENTS

Gaps 0; Ouery Match

Social Similarity 67.7%; Pred. No. 3.4e-34;
Matches 63; Conservative 12; Mismatches 18; Indels

0;

1 MAVIALKPYDFPVKDAVEKFPAPLLYVCWENHLMFPAPFCLPLPPDMPFGALAGDVLPPV 60 g  $\delta \Delta$ 

61 YGYHPDFAKIDWDRVEWFRSGEPWAPDPAKSLA 93 QY

61 QQ

RESULT W98974

AC DI

W98974 standard; Frotein; 119 AA. W98974; 10-MAY-1999 (first entry) Alcaligenes sp. protein PoxE.

Qγ

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Mammalian cell with reduced activity of low Km hexokinase - caused
80 KDLLEKFNAVPIFLSDE-
                                                                                                                                                                                                                                                   glucose; glucokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 97-385343/35.
N-PSDB; V00084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Becker TC, Han H, WPI; 97-385327/35. N-PSDB; V00136.
                                                                                                                                                                                     17-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                         invention also describes PoxA, PoxB, PoxC, PoxC, PoxE. The present and PoxI. The proteins are useful in the fields of petroleum purification, chemical industry and drug industry related to the synthesis, conversion and decomposition of accomposition of accompos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trehalose synthase structural genes - used to improve stress tolerance in e.g. plant cells, to increase storage life of foodstuffs, and for industrial prodn. of trehalose claim 1; Page 83-84; 156pp; English.
TSS1 is involved in the expression of both TPS (Trehalose-6-phosphate synthase) and TPP (Trehalose-6-phosphate phosphatase) catalytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trehalose synthase; trehalose-6-phosphate synthase; TPS; trehalose-6-phosphate phosphatase; TPP; TSS1; TSL1; stress tolerance; plant cells; foodstuffs; storage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 KDAVEKFPAPLLYVCWENHLMFPAPFCLPLPPDMPFGALAGDVLPPVYGYHPDFAKIDWD 73
       Alcaligenes; PoxR; PoxB; PoxB; PoxC; PoxD; PoxE; PoxF; PoxG; PoxH; PoxI; aromatic; oxidative; petroleum purification; chemical industry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                       useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAVIALKPYDFPVKDAVEKFPA-PLLYVCWENHLMFPAPFCLPLPPDMPFGALAGDVLPP 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 VYGYHPDFAKIDWDRVEWFRSGEPWAPDPAKSLAGNGLGHKDLISFRTPGLDGLGGAS 117
                                                                                                                                                                                                                                                     New encoding an aromatic cpd, oxidative decompsn, enzyme - useful i
the fields of petroleum purification, chemical and drug industries
Claim 1; Page 7-19; 35pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.8%; Score 78.5; DB 1; Length 495; 24.7%; Pred No. 0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.3%; Score 341.5; DB 1
53.4%; Pred. No. 6.6e-31;
Live 13; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Mismatches
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              Alcaligenes; PoxR; PoxA; PoxB; PoxC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R41362 standard; Protein; 495 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63; Conservative
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14-FEB-1992; US-836021.
28-FEB-1992; US-841997.
                                                                                                                                                                       25-JUL-1997; JP-200625.
                                                                                                                                                                                            (TOFU ) TONEN CORP. WPI; 99-197820/17.
                                                                                                                          16-FEB-1999.
25-JUL-1997; 200625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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(ALKO-) ALKO OY AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Londesborough J, WPI; 93-288399/36.
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                                                                                  Alcaligenes sp.
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                                                                                                                                                                                                                    WPI; 99-197820
N-PSDB; X18867
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Mammalian cell with reduced activity of low Km hexokinase - caused by competitive enzyme inhibitor, particularly an insulin secreting cell for in vitro or in a competitive inhibitor or in vitro includes enough of a mammalian cell has been developed which includes enough of a mammalian cell has been developed which includes enough of a reduce the hexokinase activity in the cell. The present sequence represents trehalose-6-phosphate synthase used in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trehalose-6-phosphate synthase.
Hexokinase; competitive enzyme; inhibitor; insulin; diabetes; B cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The cells are particularly used to produce insulin, in response to glucose or other secretagogues, either in vitro or in vivo (for treating diabetes), but may also be used to produce many other therapeutic proteins, e.g. from a gene under control of the insulin promoter and thus responsive to glucose. Inhibition of the inhibitor can be used more generally to reduce the growth rate of cells, e.g. sequence 495 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 KDAVEKFPAPLLYVCWENHLMFPAPFCLPLPPDMPFGALAGDVLPPVYGYHPDFAKIDWD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.8%; Score 78.5; DB 1; Length 495; 24.7%; Pred. No. 0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          trehalose-6-phosphate synthase; hexokinase; ribozyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Normington KD, Thigpen AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Newgard CB, Wilson JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 ENAWEGYNEANQIFTNEIAKT-----MNHNDLI 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAR-1998 (first entry)
Yeast trehalose-6-phosphate synthase.
Yeast; trehalose-6-phosphate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W37427 standard; Protein; 495 AA.
   AA.
                                                                                                                                                                                                                                                                                               24-012-1397; U00786.
17-JAN-1997; U00786.
19-JAN-1996; US-588976.
(BETA-) BETAGENE INC.
(UNR) JUNY MICHIGAN STATE.
(TEXA ) UNIY TEXAS SYSTEM.
BECKET TC, Han H, Newgard CB
W37441 standard; Protein; 495
W37441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae.
W09726357-A1.
24-UL-1997.
17-JAN-1997; U00787.
19-JAN-1996; US-588983.
(BETA) BETAGENE INC.
(TEXA) UNIV TEXAS SYSTEM.
Han H, Newgard CB, Normins
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.85
Best Local Similarity 24.77
Matches 23; Conservative
                                                                                                                                                                                                         Saccharomyces cerevisiae.
WO9726322-A2.
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RESULT
W64591
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                                                                                                                                                                                                                                                                                                                                                                                                  4;
by specific ribozyme or stimulator of trehalose-6-phosphate production, particularly for in vitro or in vivo insulin production Claim 13; Page 152-154; 265pp; English.

A mammalian cell has been developed comprising an effective amount of a low Km hexokinase-inhibitor selected from: (a) an agent that stimulates production of trehalose-6-phosphate (16P); or (b) a ribozyme specific for low Km hexokinase. The present sequence represents yeast trehalose-6-phosphate synthase. The cells are particularly used to
                                                                                                                              produce insulin, in response to glucose or other secretagogues, cither in vivo (for treating diabetes), but may also be used to produce many other therapeutic proteins, e.g. from a gene under control of the insulin promoter which is therefore responsive to glucose. Growth-inhibited cells (having altered haxokinase activity) are used to Produce proteins, e.g. insulin or antibodies, in vivo or in vitro. Reduction in low Km hexokinase activity provides cells in which insulin secretion is induced at glucose concentrations closer to the normal range than in the parent cell (nearly homeostatic secretion). Implanted cells of reduced low Km hexokinase activity are expected to survive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a fragment of a human protein which contains a SRCR (scavenger receptor, cysteine-rich) domain. The gene and encoded protein can be used to diagnose or treat tumours, particularly of the nervous system (medullo-blastoma or glioma) or breast. The DNA sequence and probes derived from it, are used to identify genes that express SRCR-domain containing proteins, to determine the form in which these proteins exist and to assess the significance of individual forms on cellular properties. The protein can be used to detect the presence of sequence 666 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human SRCR protein fragment.
Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment;
nervous system; medullo blastoma; glioma; breast; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                      14 KDAVEKFPAPLLYVCWENHLMFPAPFCLPLPDMPFGALAGDVLPPVYGYHPDFAKIDWD 73
                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteins containing scavenger receptor, cysteine rich domain
                                                                                                                                                                                                                                                                                                                                                                 Length 495;
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                           28;
                                                                                                                                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for diagnosis and treatment of tumours
                                                                                                                                                                                                                                                                                                                                                            Score 78.5; DB
Pred. No. 0.59;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 RVEWF---RSGEPWAPDPAKSLAGNGLGHKDLI 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W64590 standard; Protein; 666
                                                                                                                                                                                                                                                                                                                                                            11.8%;
24.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 54pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                             80 KDLLEKFNAVPIFLSDE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                           23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mollenhauer J, Poustka A;
WPI; 98-399136/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUL-1997; DE-030997.
09-JAN-1997; DE-000519.
                                                                                                                                                                                                                                                                                              longer in the host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JAN-1998; D00096.
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; V49651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9830687-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoantibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUL-1998.
                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W64590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W64590
   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents a human protein which contains a SRCR (scavenger receptor, cysteine-rich) domain. The gene and encoded protein can be used to diagnose or treat tumnours, particularly of the nervous system (medullo-blastoma or glioma) or breast. The DNA sequence and probes containing proteins, to determine the form in which these proteins exist properties. The significance of individual forms on cellular proteins can be used to detect the presence of autoanticodies and antibodies which regulate its expression.
                                Gaps
                                                                                                                                                                                                                                                                                       Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment; nervous system; medullo-blastoma; glioma; breast; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGS1 glucose sensing protein.
Glucose; sensing; cell signalling; yeast; Saccharomyces cerevisiae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1356 ICSGNHLSTPAPFLNITRPNTDYSCGGFLSQPSGDFSSPFYPGNYPNNAKCVWD 1409
                                                                                        405 ICSGNHLSTPAPPELNITRPNTDYSCGGFLSQPSGDFSSPFYPGNYPNNAKCVWD 458
                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                          27 VCWENHLMFPAPFCLPLPPDMPF---GAL---AGDVLPPVY-GYHPDFAKIDWD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 VCWENHLMFPAPFCLPLPPDMPF---GAL---AGDVLPPVY-GYHPDFAKIDWD 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1785;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins containing scavenger receptor, cysteine rich domain useful for diagnosis and treatment of tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              beverage; brewing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transformed yeast with increased stress resistance or fermentation capacity - has modification in general glucose sensor system, partic, for bread-making, but also prodn. of alcohol or foreign proteins
                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           freezing; sugar metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.2%; Score 74.5; DB 1; 38.9%; Pred. No. 7.5;
    Pred. No. 2.3;
                       6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bread; breadmaking; fermentation; alcohol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUL-1992; 870102.

09-JUL-1992; EP-870102.

(ALGI.) ALGIST-BRUGGENAN NV.

Hohmann S. Thevelein J, Van Dijck P;

WPI; 94-009855/02.

N-PSDB; Q54385.
                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-1997; DE-030997.
09-JAN-1997; DE-000519.
(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                         W64591 standard; Protein; 1785 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R44923 standard; Protein; 495 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 2; 54pp; German.
  38.98;
                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mollenhauer J, Poustka A;
WPI; 98-399136/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 38.9 les 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           drying; osmotic shock;
                                                                                                                                                                                                                                                                                                                                                                                                16-JUL-1998.
09-JAN-1998; D00096.
                                                                                                                                                                                                                                                                      Human SRCR protein.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1785 AA;
                                                                                                                                                                                                                                                                                                                                     autoantibody; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; V49652
                                                                                                                                                                                                                                                                                                                                                                            W09830687-A2.
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                23-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-1994.
                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP-577915-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
                                                                                                                                                                                                                                 W64591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R44923
                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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103

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74 RVEWF -- - RSGEPWAPDPAKSLAGNGLGHKDLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R14408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                   q
                                                                                                                                                             ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                    δλ
                                                                                                                                                                                                                                   4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents the Saccharomyces cerevisiae trehalose synthase. The invention provides methods of preserving prokaryotic cells which involves inducing the intracellular trehalose production of the prokaryotic cell to an amount which effectively allows increased storage stability and drying of the cells in the presence of a stabilising agent. Therefore, prokaryotic cells known to synthesise trahalose, such as S. cerevisiae, can be used to illustrate the methods of the invention. Bacteria tabilised by these methods showed less than 10% loss of viability on storage even after being stored at temperatures up to at least 37 degrees centigrade for as long as 6 weeks. The invention claims the methods to be useful for producing dried, stable probaryotic cells such as bacteria useful for pharmacological treatment, prophylaxis, agricultural and industrial applications. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             also claims the methods to be useful for producing live bacterial vaccines in a dry stable form, live bacterial neutraceuticals in a dry stable form and other live bacterial pharmaceuticals in a dry stable form, e.g. for treatment of vaginal or urinary tract infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae trehalose synthase. Trehalose synthase, stabilising agent; prokaryotic cell preservation; prophylaxis; live bacterial vaccine; vaginal infection; urinary tract infection; live bacterial neutraceutical.
                                                                                                                                                                                                                                                                                        Disclosure; Figure 1; 26pp; French.
Yeast strains transformed with an altered GGS1 gene are resistant to stress and/or have an altered sugar metabolism. The transformed yeast can be used in industry for the production of bread, alcohol and beverages and has resistance to at least one of drying, osmotic shock (especially in sugar containing doughs) and freezing.

Preferably the yeast also has higher trehalose content with delayed trehalose mobilisation.
                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Preservation of prokaryotic cells - by increasing intracellular trehalose concentration, mixing with a stabilising agent, and drying to produce a glass form of the stabilising agent Disclosure; Pages 39-40; 64pp; English.
                                                                                                                                                                                                                                                                  KDAVEKFPAPLLXVCWENHLMFPAPFCLPLPPDMPFGALAGDVLPPVYGYHPDFAKIDWD 73
                                                                                                                                                                                                                                   23;
                                                                                                                                                                                              DB 1; Length 495;
                                                                                                                                                                                                                                 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colaco C, Dhaliwal KS, Roser BJ, Tunnacliffe AG,
                                                                                                                                                                                              10.9%; Score 72.5; DE 23.7%; Pred. No. 2.7; ive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                        74 RVEWF---RSGEPWAPDPAKSLAGNGLGHKDLI 103
                                                                                                                                                                                                                                                                                                                                                                         125 ENAWLAYNEANQTFINEIAKT-----MNHNDLI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (QUAD-) QUADRANT HOLDINGS CAMBRIDGE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W49026 standard; protein; 495 AA.
                                                                                                                                                                                                                                                                                                         80 KDLLEKFNAVPIFLSDE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomyces cerevisiae W09824882-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-1997; G03375.
05-DEC-1996; US-032423.
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98-333305/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-0CT-1998
                                                                                                                                                                                                                                   22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Welsh DT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                Query Match
Best Local S
                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W49026
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
W49026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   & 555555558
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83 VLYIKAKSFPAQGSPAQAPEPGL---WNTNLLVKTDRRLYDFDLVLASADAATPQALQRS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 ------APFCLPLPPDMPFGAL-----AGDVLPPVYGYHPDFAKI 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The
                                                                                                                                                                                                                                                                                                                                                                                                                         microorganisms transformed with Bordetella pertussis ptx operon and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 RMAYRIQFRYPAAPQAASRASPVGPAVPAGALNRRYAMQVGNGSDGIAPIAAY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella pertussis ptsE.
Holotoxin; ptx; pts; gene; extracellular export; ptsE; secretion; whooping cough; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 DWDRVEW--FRSGEPW-----APDPAKSLAGNGLGHKDLISFR-TPGLDGLGGAS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1: Columns 45-48; 33pp; English.

The present sequence is the Bordetella pertussis ptsE, which is 1 of the proteins encoded by the pts gene that facilitate the extracellular export of the pertussis holotoxin (ptx), namely ptsAB, ptsC, ptsB, ptsE, and ptsG. A secreted ptx can be produced by culturing an E. coli or Bordetella host transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          operatively linked to appropriate expression control sequences. secreted ptx can be used in the production of whooping cough
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                       Production of secreted pertussis holotoxin - by culturing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with 1 or more vectors, comprising the ptx and pts genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear factor C/EBP2.
Interleukin 6; IL-6; transcription; hematinic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 71.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VIALKPYDFPVKDAVEKFPAPLLYVCWENHLM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R14408 standard; Protein; 345 AA
                                          W23277 standard; Protein; 273 AA.
                                                                                                                                                                                                                                                                                                              (AMCY ) AMERICAN CYANAMID CO.
Baker SM, Deich RA;
WPI; 97-350237/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      new pts secretion sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-DEC-1989; JP-336868.
17-OCT-1990; JP-279650.
(CHGZ-) CHUZO KISH IMOTO.
WPI: 91-351133/48.
N-PSDB; Q15015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-FEB-1992 (first entry)
                                                                                    03-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 21.6
Matches 38; Conservative
                                                                                                                                                                                                                                                                 31-MAR-1994; US-221750.
15-MAR-1993; US-031619.
                                                                                                                                                                             Bordetella pertussis
                                                                                                                                                                                                                         01-JUL-1997.
15-MAR-1993; 031619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 AA;
                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; T84745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
J03236782-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-0CT-1990
                                                                                                                                                                                                    US5643747-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccines
RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID
DT
DT
DE
PR
PR
DR
DR
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4;

23; Gaps

Indels

29;

19; Mismatches

Conservative

22;

Matches

Qγ

Local Similarity

Query Match Best Local S

14 KDAVEKEPAPLLYVCWENHLMFPAPFCLPLPPDMPFGALAGDVLPPVYGYHPDFAKIDWD 73

10.9%; Score 72.5; DB 1; Length 495; 23.7%; Pred. No. 2.7;

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                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 ENHLMFPAPFCLPLPPDMP--FGALAGDV--LPPVY---GYHPDFAKIDWDRVEWFRSGE 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-062-1996 (first entry)
Human interleukin-11 receptor.
Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;
                                             Claim 6; Page 7; 20pp; Japanese.

The sequence was deduced from a gene isolated from a library prepd.

Trom human peripheral blood monocyte cDNA. Recombinant C/EBP2 is useful as a hematinic.

Sequence 345 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB: 063879.

DNA encoding poly-hydroxy-alkanoate decomposing enzyme - useful for preparing poly-hydroxy-alkanoate in large quantities claim 3; page 13-14; 15pp; Japanese.

K63805 is encoded by ORF 2 of 063789, which produces a polypeptide which shows polyhydroxyalkanoate decomposing activity. The method used allows the polypeptide to be prepared in large quantities.
 Nuclear factor of gene expressing and deriving IL 6 gene - codes factor combined sequence of structure for transcriptional control
                                                                                                                                                                                                                                       65 PDFAKI----DWDRVEWFRS-----GEPWAPDPAKSL---------AGNGLGH--
                                                                                                                                                                                                                       ----FGALAGDVLPPVY--GYH
                                                                                                                                                                                            61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
                                                                                                                                                        10.0%; Score 66.5; DB 1; Length 345; 24.8%; Pred. No. 8.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.8%; Score 65; DB 1; Length 261; 32.1%; Pred. No. 8.8;
                                                                                                                                                                                         35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polyhydroxyalkanoate decomposing activity polypeptide.
Polyhydroxyalkanoate decomposing enzyme; PHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-SEP-1992; 279099.
07-SEP-1992; JP-279099.
07-SEP-1992; JP-279099.
(UKEA) DENKI KAGAKU KOGYO KK.
(UKKA-) GF KANAGAWA DAIGAKU.
(CHIKA-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
WPI; 94-140539/17.
                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  R63805 standard; Protein; 261 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R99090 standard; Protein; 422 AA.
                                                                                                                                                                                                                    27 VCWENHLMFPAPFCLPLPPDMP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 PWAPDPAKSLAGNGLGHK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 --APLPA----DGLGHR 143
                                                                                                                                                                                                                                                                                                                                         100 -KDLISFRTPGLDGLGG 115
                                                                                                                                                                                                                                                                                                                                                                        118 LSDLFS-----DDYGG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-1994 (first entry)
                                                                                                                                                                     Local Similarity 24.8 ses 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
'-hag 25; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zoogloea ramigera.
J06086681-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-MAR-1994
                                   dene
                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R63805;
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Matches
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New nucleic acid encoding human interleukin 11 receptor - and related protein, antibodies, receptor antagonists, etc, useful for treating and preventing loss of bone mass claim 13, Page 35-37; 54pp; English.

Claim 13, Page 35-37; 54pp; English.

C Human interleukin-11 (IL-11) receptor (R99090) is thought to play a role in the regulation of bone maturation and repair. Its amino acid sequence was deduced form a cDNA clone (T3378) isolated from a human activated peripheral blood mononuclear cell cDNA library.

C Recombinant IL-11 receptor or its fragments, pref. amino acids 24-422, 24-365 (soluble extracellular domain), 391-422, 102-422 or treat/prevent loss of bone mass (e.g. osteoporosis, Paget's disease, multiple myeloma or hypogonadal conditions), as well as immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human interleukin-11 recéptor alpha chain.
Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 DRVEWFRSGEPWAPDPAKSLAG--NGLGHK------DLISFRTPGLDG-LGG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label Extracellular_domain
/note= "the extracellular domain includes
haemopoietin and Ig-like domains"
                                                                                                                                                /label= Type-1-cytokine_region 366. .390
                                                                                                                                                         366. 390
/label= Transmembrane_domain
391. .422
                                                                                                   /label= Extracellular_domain
                                                                                                                                                                                                          /label= Intracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Transmembrane_domain 393. .423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches
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/label= Cytoplasmic_tail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.8%; Score 65; 40.0%; Pred. No.
                                                                                                                             /label= Ig-like_region
osteoporosis; Paget disease; myeloma.
                                       1. .23
/label= Sig_peptide
                                                               24. .422
/label= Mat_protein
24. .365
                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .23
/label= Sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R92814 standard; Protein; 423 AA.
                                                                                                                                            .365
                                                                                                                                                                                                                                                                        GENETICS INST INC.
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                                                                                                                    .111
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                                                                                                                                                                                                                                                           US-362304
                                                                                                                                                                                                                                  27-JUN-1996.
27-NOV-1995; U15400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy; diagnosis.
Homo sapiens.
                                                                                                                                                                                                                                                                                                 WPI; 96-309588/31.
                                                                                                                                                                                                                                                                                                              N-PSDB; T33278
              Homo sapiens.
                                                                                                                                                                                                                      WO9619574-A1.
                                                                                                                                                                                                                                                           22-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY-1996
                                                                                                                                                                                                                                                                                    Tobin JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                     peptide
                                                               protein
                                                                                                                                                                                                                                                                          (GEMY)
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Matches
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R92814
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4;
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This sequence represents a human papillary renal cell carcinoma (PRCC) associated protein and is used in a method for the diagnosis.

prophylactic and therapeutic treatment of papillary renal cell carcinoma. The translocation t(X:1) (pl1.2:q21.2) found in PRCC results in a fusion of the transcription factor, TFB3 quee with a new chromosome I gene designated PRCC (at 1q21.2), resulting in expression of a fusion protein Normal TFB3 transcripts are no longer produced. Two other fusion partners for TFB3 have also been detected; Non0, from a invX (pl1.2; q13-24 or 12) translocation and the PSF splice factor gene, resulting in t(X:1) encountered in patients younger than 25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18; Gaps
                                                                                                                                                 Nucleic acid encoding haemopoietin receptor containing conserved amino acid encoding haemopoietin receptor alpha chain - used for developing IL-II (ant)agonists
Claim 8; Page 47-49; 87pp; English.
The human interleukin-II (IL-II) receptor alpha chain (R92814)
was identified by expression of DNA (17869) isolated from human bone marrow cDNA libraries. Expression of the human IL-II
and permits IL-II signalling. The receptor alpha chain can be used to develop agonists or antagonists of therapeutic appla.
The treatment or diagnosis of conditions involving a deficiency of IL-II, excess IL-II or aberrant effects of normal endogenous IL-II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Diagnosing papillary renal cell carcinoma by detecting gene trans-location - resulting in fusion of FPE3 gene with some other gene, also related vectors, transformed cells, specific binding reagents, peptide(s) encoded by fusions and therapeutic anti-sense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human chromosome I PRCC associated protein.
PRCC, papillary renal cell carcinoma; TFE3; transcription factor;
fusion protein; translocation; diagnosis; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 DRVEWFRSGEPWAPDPAKSLAG--NGLGHK------DLISFRIPGLDG-LGG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55 DPVSWFRDGEP-----KLLQGPDSGLGHELVLAQADSTDEGTYICQTLDGALGG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 1; Length 423;
Pred. No. 15;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
Clark J, Cooper C, Shipley J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W52826 standard; Protein; 491 AA.
                                                                        05-SEP-1994; AU-007901.
(AMRA-) AMRAD OPERATIONS PTY LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 40.0
Matches 22; Conservative
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13-AUG-1997; G02209.
13-AUG-1996; GB-016986.
                                                        05-SEP-1994; AU-007902.
                  14-MAR-1996.
05-SEP-1995; AU0578.
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N-PSDB; V20962.
                                                                                                                                  96-171612/17.
                                                                                                                                                                                                                                                                                                                                                                                                                          423 AA;
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WO9806871-A1.
                                                                                                                Hilton DJ;
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DB 1; Length 491;

9.8%; Score 65;

Query Match

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62 FPPPLLLLPPPTGDPRLQPPPLPFG-LGG--FPPPPGVSP-----AEAAGVGE--- 106
                      Gaps
                                                   35 FPAPFCLP-----LPPDMPFGALAGDVLPPVYGYHPDFAKIDWDRVEWFRSGEPWA 85
                    38;
                   21; Indels
                                                                                                                       86 PDPAKSLAGNGLGHKDLISFRTPGLD---GLGGA 116
                                                                                                                                        Pred. No. 18;
3; Mismatches
                                                                                                                                                                                                                     Search completed: September 26, 2000, 20:11:52 Job time: 10376 sec
      34.0%;
                      32; Conservative
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                        107
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                                                         Qγ
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